



# ***STIC Search Report***

## ***Biotech-Chem Library***

**STIC Database Tracking Number: 184731**

**TO: Minh-Tam Davis**  
**Location: REM/3a24/3c18**  
**Art Unit: 1642**

*April 12* 2006

**Case Serial Number: 09/277064**

**From: P. Sheppard**  
**Location: Remsen Building**  
**Phone: (571) 272-2529**

**sheppard@uspto.gov**

### **Search Notes**

73622  
STIC-Biotech/ChemLib

184731

ME

From: Chan, Christina  
Sent: Monday, April 10, 2006 8:16 AM  
To: Davis, Minh-Tam; STIC-Biotech/ChemLib  
Subject: RE: Rush search request for 09/277064

Please ~~rush~~. Thanks Chris

Chris Chan  
TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

RECEIVED  
APR 10 2006  
STIC

-----Original Message-----

From: Davis, Minh-Tam  
Sent: Friday, April 07, 2006 12:27 PM  
To: Chan, Christina  
Subject: Rush search request for 09/277064

Please search in commercial database, issued patent files and PGPUB:  
SEQ ID NO:12, with size limitation to the size of the sequence.  
Thank you.  
MINH TAM DAVIS  
ART UNIT 1642, ROOM 3A24, MB 3C18  
27-0830

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2006, 19:27:15 ; Search time 188 Seconds  
(without alignments)  
23.371 Million cell updates/sec

Title: US-09-277-064-12

Perfect score: 51

Sequence: 1 VMAGVGSFV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21:\*

1: geneseq1980s:\*

2: geneseq1990s:\*

3: geneseq2000s:\*

4: geneseq2001s:\*

5: geneseq2002s:\*

6: geneseq2003as:\*

7: geneseq2003bs:\*

8: geneseq2004s:\*

9: geneseq2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	2 AAR61525	Aar61525 Peptide f
2	51	100.0	10	2 AAR97508	Aar97508 Cytotoxic
3	51	100.0	10	2 AAW36826	Aaw36826 Immunogen
4	51	100.0	10	2 AAW70071	Aaw70071 HER-2/neu
5	51	100.0	10	2 AAW77132	Aaw77132 HER-2/neu
6	51	100.0	10	4 AAB99690	Aab99690 HLA A2 bi
7	51	100.0	10	4 AAB89003	Aag89003 HER2/neu
8	51	100.0	10	4 AAG88772	Aag88772 HER2/neu
9	51	100.0	10	5 AAB76755	Abb76755 Tumour an
10	51	100.0	10	5 AAE26800	Aae26800 Human HLA
11	51	100.0	10	5 AEA36306	Aea36306 Human HER
12	51	100.0	10	6 ABU63012	Abu63012 Human Her
13	51	100.0	10	8 ADE97756	Ade97756 Immunogen
14	51	100.0	10	8 ADM12647	Adm12647 MHC class
15	51	100.0	10	8 ADO38880	Ado38880 Human Her
16	51	100.0	10	8 ADP79761	Adp79761 Human HLA
17	51	100.0	15	3 AAY98861	Aay98861 HLA class
18	51	100.0	15	4 AAG88322	Aag88322 HER2/NEU
19	51	100.0	15	4 AAG88306	Aag88306 HER2/NEU
20	51	100.0	15	4 AAG89058	Aag89058 HER2/neu
21	51	100.0	15	4 AAG89031	Aag89031 Her2/neu
22	51	100.0	15	4 AAG89114	Aag89114 HER2/neu
23	51	100.0	18	5 ABJ04191	Abj04191 Kinase-as
24	51	100.0	18	6 ABU54238	Abu54238 ErbB2 pro

25	51	100.0	18	8 ADK72373	Adk72373 HER-2 pep
26	51	100.0	22	8 ADM12649	Adm12649 Ii-key/hu
27	51	100.0	22	8 ADO38882	Ado38882 Human Her
28	51	100.0	112	8 ADK72377	Adk72377 Human HER
29	51	100.0	265	2 AAY43967	Aay43967 Human pro
30	51	100.0	289	8 ADS87905	Ads87905 HER2/Erbb
31	51	100.0	391	9 AEA39008	Aea39008 Rat Her-2
32	51	100.0	435	9 ADR10480	Adr10480 Human pro
33	51	100.0	470	9 ADY30515	Ady30515 Human epl
34	51	100.0	550	8 ADP80498	Adp80498 Human epl
35	51	100.0	583	5 AAE20483	Aae20483 Human pro
36	51	100.0	587	5 AAE20481	Aae20481 Human pro
37	51	100.0	589	5 AAE20484	Aae20484 Human pro
38	51	100.0	600	5 AAE20482	Aae20482 Human pro
39	51	100.0	671	8 ADK72375	Adk72375 BCG-HER-2
40	51	100.0	815	8 ADT50879	Adt50879 Cancer re
41	51	100.0	835	9 ADY30511	Ady30511 Human epl
42	51	100.0	879	9 ADY30514	Ady30514 Human epl
43	51	100.0	960	9 ADY30513	Ady30513 Human epl
44	51	100.0	970	9 ADY30509	Ady30509 Human epl
45	51	100.0	1042	7 ADM29352	Adm29352 Human nov

## ALIGNMENTS

RESULT 1  
AAR61525

ID AAR61525 standard; peptide; 10 AA.

XX AAR61525;

XX 25-MAR-2003 (revised)

DT 11-MAY-1995 (first entry)

XX Peptide fragment (1.0738) of c-ERB2 binds HLA-A2.1.

XX antigen; epitope; immunogenic target protein; PSA; HBVC; HBVs; EBV; HIV1;  
XX plasma specific antigen; hepatitis B virus; Epstein Barr;  
XX human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1;  
XX melanoma antigen-1; core antigen; surface antigen;  
XX pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;  
XX MHC class I molecule; major histocompatibility complex; HLA-A2.1; 9mer;  
XX 10mer; anchor; human leukocyte antigen.

XX Homo sapiens.

XX OS WO9420127-A1.

XX PD 15-SEP-1994.

XX PF 04-MAR-1994; 94WO-US002353.

XX PR 05-MAR-1993; 93US-00027146.

XX PR 04-JUN-1993; 93US-00073205.

XX PR 29-NOV-1993; 93US-00159184.

XX (CYTE-) CYTEL CORP.

XX Grey HM, Sette A, Sidney J, Kast W;

XX WPI; 1994-302678/37.

XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for  
XX treatment or prophylaxis of cancer, virus infection or autoimmune  
XX diseases.

XX Example 5; Page 108; 138pp; English.

XX AAR59496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1  
XX binding motif. These peptides bind HLA-A2.1 and have a binding affinity  
XX of at least 1% as compared to a reference peptide (AAR71293). AAR61525  
XX has an IC50 of 0.018 and the sequence occurs at position 773 in the human

CC c-erbB2 gene product. Peptides of the invention can induce cytotoxic T  
CC lymphocytes which can react with target cells. They can be used for the  
CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma, etc.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 10 AA;

Query Match 100.0%; Score 51; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VMAGVGSPYV 10  
DB 1 VMAGVGSPYV 10  
|||||

## RESULT 2

AAR97508  
ID AAR97508 standard; peptide; 10 AA.

XX  
AC AAR97508;

XX 11-FEB-1997 (first entry)

XX Cytotoxic T lymphocyte-activating Her-2/Neu-specific peptide.

XX p53; Her-2; Neu; aa; amino acid; CTL; cytotoxic T lymphocyte; target;  
KW malignant cell; antigenic; vaccine; immunisation; activation.  
XX  
XX Homo sapiens.

OS  
PN WO9618409-A1.

XX  
PD 20-JUN-1996.

XX 14-DEC-1995; 95WO-US016415.

XX 14-DEC-1994; 94US-00355558.

XX (SCRI ) SCRIPPS RES INST.

XX Sherman LA;

XX WPI; 1996-300385/30.

XX In vivo activation of tumour-specific cytotoxic T lymphocytes - by  
PT contacting with polypeptide(s) derived from human p53 or Her-2/Neu  
PT proteins.

XX Claim 5; Page 124; 158pp; English.

XX AAR97508 is a peptide capable of activating cytotoxic T lymphocytes  
CC (CTLs) which specifically target malignant cells. The peptide corresponds  
CC to amino acids 773-792 of human Her-2/Neu protein. CTL-activating  
CC peptides can be used in a vaccine for protecting against tumour cell  
CC formation. CTLs activated by the peptides will lyse tumour cells  
CC displaying specific peptides. Antibodies against CTL-activating peptides  
CC are useful for the identification of other similar compounds which may be  
CC useful for treating cancer or virally-infected cells, or for diagnosis.  
CC The peptide and vaccines produced provide immunity to a high percentage  
CC of different ethnic groups, i.e. those with different HLA alleles  
XX

XX Sequence 10 AA;

Query Match 100.0%; Score 51; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPYV 10

DB 1 VMAGVGSPYV 10  
|||||

## RESULT 4

AAW70071

## RESULT 3

AAW36826  
ID AAW36826 standard; peptide; 10 AA.

XX  
AC AAW36826;

XX 23-MAR-1998 (first entry)

XX Immunogenic peptide H7 based on the human Her-2/neu protein.

XX Her-2/neu protein; human leukocyte antigen A2.1; HLA;

XX cytotoxic T lymphocyte; CTL; immune response; tumour-associated antigen;

XX T-cell receptor; TCR; tumour treatment.

XX Synthetic.

OS Homo sapiens.

XX WO9732603-A1.

XX 12-SEP-1997.

XX 05-MAR-1997; 97WO-US003611.

XX 05-MAR-1996; 96US-0012845P.

XX (SCRI ) SCRIPPS RES INST.

XX Sherman LA, Lustgarten J;

XX WPI; 1997-470496/43.

XX Nucleic acid encoding variable regions of HLA-restricted non-human T cell  
PT receptor specific for tumour antigen - used to identify tumour antigens  
PT and for tumour therapy.

XX Example 1; Page 9; 34pp; English.

XX Synthetic peptides AAW36824-40 are based on the sequence of the human Her  
CC -2/neu protein, wherein each sequence contains the anchor motif for human  
CC leukocyte antigen (HLA) A2.1. The present peptide is based on positions  
CC 773-782. The ability of these peptides to inhibit the binding of an  
CC influenza virus matrix protein peptide M1 to HLA A2.1 was measured by  
CC inhibition of lysis by an M1 specific, HLA A2.1 restricted, cytotoxic T  
CC lymphocyte (CTL) clone. The present protein showed 58% inhibition. The  
CC peptides were also tested for their ability to elicit an immune response  
CC in vivo. However, only H3 (AAW36824) and H7 (AAW36826) were able to do  
CC this. H3 and H7 peptides are tumour-associated antigens, and were used to  
CC immunize a transgenic, non-human vertebrate (that has been modified to  
CC express at least one HLA antigen), so that the animal produces CTL which  
CC displays HLA-restricted T-cell receptor (TCR) specificity for the  
CC antigen. Nucleic acid encoding variable regions of the alpha and beta  
CC chains of such TCRs can be amplified from CTLs produced in the above  
CC manner. Cells expressing recombinant TCR are used to identify antigens  
CC associated with a tumour and to treat tumours in humans. Transgenic mice  
CC are a more convenient source of CTL than the tumour-infiltrating  
CC lymphocytes previously used. TCR can be humanised to reduce side-  
CC reactions and short peptide derivatives of TCR are more economical to  
CC produce than TCR itself, particularly when expressed as a single-chain  
CC molecule rather than as a dimer  
XX

XX Sequence 10 AA;

Query Match 100.0%; Score 51; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPYV 10

DB 1 VMAGVGSPYV 10  
|||||

ID AAW70071 standard; peptide; 10 AA.  
 AC AAW70071;  
 XX  
 DT 22-OCT-1998 (first entry)  
 DE HER-2/neu derived HLA-A2.1 binding peptide 19 (residues 773-782).  
 DE  
 KW Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;  
 KW human leukocyte antigen; HLA; tumour associated antigen; cancer;  
 KW antigen presenting cell; APC; immunogenic peptide; immune disorder;  
 KW viral infection; AIDS; hepatitis; bacterial infection; malaria;  
 KW fungal infection; tuberculosis; melanoma; HER-2/neu; cerB-2.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9833888-A1.  
 XX  
 XX 06-AUG-1998.  
 PD  
 XX  
 PF 30-JAN-1998; 98WO-US001959.  
 XX  
 PR 31-JAN-1997; 97US-0036696P.  
 XX  
 XX (EPIM-) EPIMUNE INC.  
 PA  
 XX Tsai V, Southwood S, Sidney J, Sette A, Celis E;  
 PI WPI; 1998-437445/37.  
 DR  
 XX  
 XX Production of antigen-specific cytotoxic T cells - by incubating  
 PT immunogenic peptide(s) from antigen that binds class I major  
 PT histocompatibility complex molecules with pre-treated antigen presenting  
 PT cells.  
 XX  
 XX Example 7; Page 77; 104pp; English.  
 PS  
 XX  
 XX Sequences shown in AAW70053 to AAW70075 represent peptides derived from  
 CC HER-2/neu (cerB-2) antigen. The peptides can bind to a human leukocyte  
 CC antigen (HLA), HLA-A2.1 and are used to exemplify the method of invention  
 CC of producing antigen-specific cytotoxic T cells (CTLs) in vitro. The  
 CC method comprises contacting immunogenic peptides from an antigen that  
 CC binds class I major histocompatibility complex (MHC) molecules with  
 CC antigen presenting cells (APCs) pretreated with pretreatment growth  
 CC factors, and incubating the APCs with purified CD8 cells in the presence  
 CC of at least 2 incubation growth factors, thereby producing antigen-  
 CC specific CTLs. A method for specifically killing target cells in a human  
 CC patient is also provided which comprises obtaining a fluid sample  
 CC containing CTLs from a patient, contacting the cytotoxic T cells with  
 CC APCs pretreated with pre-treatment growth factors, where the APCs  
 CC comprise class I MHC molecules. The pretreated APCs are incubated with  
 CC the cytotoxic growth factors, thereby producing activated CTLs which are  
 CC contacted with a carrier to form a composition. The composition can then  
 CC be administered to the patient. The activated CTLs can be used for  
 CC treating cancers, immune disorders, viral infections, AIDS, hepatitis,  
 CC bacterial infection, fungal infection, malaria or tuberculosis  
 XX  
 XX Sequence 10 AA;  
 XX  
 Query Match 100.0%; Score 51; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VMAGVGSPPV 10  
 Db 1 VMAGVGSPPV 10  
 RESULT 6  
 AAB99690  
 ID AAB99690 standard; peptide; 10 AA.  
 XX  
 AC AAB99690;  
 XX  
 DT 06-SEP-2001 (first entry)  
 DE  
 DE HLA A2 binding CTL epitope peptide from Her2/neu SEQ ID NO:11.  
 KW Human leukocyte antigen A2 binding peptide; HLA class I A2; CTL;  
 KW cytotoxic T-cell lymphocyte; tumour associated antigen; CEA; HER2/neu;  
 KW MAGE3; MAGE3; p53; vaccine; cancer; cytostatic; immunomodulator;  
 KW immunotherapy; immune response.  
 XX  
 OS Homo sapiens.  
 OS  
 XX  
 XX WO200141741-A1.  
 PN  
 XX  
 PD 14-JUN-2001.  
 XX  
 XX 13-DEC-2000; 2000WO-US034318.  
 PF  
 XX

PR 13-DEC-1999; 99US-0170448P.  
 PR 05-APR-2000; 2000US-00543608.  
 PR 30-MAY-2000; 2000US-00583200.  
 XX  
 PA (EPIM-) EPIMUNE INC.  
 XX  
 PI Fikes J, Sette A, Sidney J, Southwood S, Celis E, Keogh E;  
 PI Chesnut R;  
 XX  
 XX WPI; 2001-381489/40.  
 XX  
 XX Compositions for use in a vaccine for treating, e.g., breast, lung and  
 PT colon cancer comprises at least one peptide that comprises an isolated  
 PT epitope of a tumor-associated antigen.  
 XX  
 PS Claim 1; Page 76; 86pp; English.  
 XX  
 XX The present invention describes a composition (I) comprising at least one  
 CC peptide that comprises an isolated, prepared epitope consisting of a  
 CC sequence selected from 25 short amino acid sequences given in AAB99680 to  
 CC AAB99704. Also described are: (1) a composition (II) comprising one or  
 CC more peptides, and further comprising at least two epitopes selected from  
 CC the 25 short amino acid sequences (as above), where each of the one or  
 CC more peptides comprise less than 50 contiguous amino acids that have 100%  
 CC identity with a native peptide sequence; and (2) a vaccine composition  
 CC (III) comprising an epitope selected from the 25 short amino acid  
 CC sequences (as above) and a pharmaceutical excipient. (I) has cytostatic  
 CC and immunomodulatory activities and can be used in vaccine production and  
 CC immunotherapy. The peptide epitope compositions (I)-(II) are useful for  
 CC monitoring an immune response to a tumor associated antigen or when one  
 CC or more peptides are combined to create a vaccine (III) that stimulates  
 CC the cellular arm of the immune system. In particular, the vaccine  
 CC mediates immune responses against tumors in individuals who bear an  
 CC allele of the human leukocyte antigen (HLA)-A2 supertype and improve the  
 CC standard of care for patients being treated for breast, colon, or lung  
 CC cancer  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 51; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VMAGVGSPPV 10  
 Db |||||  
 1 VMAGVGSPPV 10  
 RESULT 7  
 AAG89003  
 ID AAG89003 standard; peptide; 10 AA.  
 AC AAG89003;  
 XX  
 DT 11-SEP-2001 (first entry)  
 XX  
 DE HER2/neu epitope HLA-A2 supermotif-bearing peptide #16.  
 KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
 KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
 KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200141787-A1.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 11-DEC-2000; 2000WO-US033591.  
 XX  
 PR 10-DEC-1999; 99US-00458299.  
 XX

PA (EPIM-) EPIMUNE INC.  
 XX  
 PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
 PI Keogh E;  
 XX  
 XX WPI; 2001-374995/39.  
 XX  
 XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
 PT cellular immune responses for the prevention and treatment of cancer.  
 PT  
 XX  
 PS Claim 1; Page 189; 199pp; English.  
 XX  
 XX The present invention describes isolated prepared HER2/neu epitopes (I).  
 CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
 CC culture in vitro and binds to a complex of an epitope (I); bound to a  
 CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
 CC and a second epitope and the peptide is less than 50 contiguous amino  
 CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
 CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
 CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
 CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
 CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
 CC (III) are useful for inducing cellular immune responses for the  
 CC prevention or treatment of cancer. (I) and (II) are useful for  
 CC monitoring or evaluating an immune response to a tumour-associated  
 CC antigen when incubated with a T lymphocyte sample from a patient and  
 CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
 CC based vaccines mean that immunosuppressive epitopes that may be present  
 CC in whole antigens may be avoided. Selected epitopes may be combined to  
 CC enhance immunogenicity. The possible pathological side effects caused by  
 CC infectious agents or whole protein antigen is eliminated. The vaccine  
 CC provides the ability to direct and focus an immune response to multiple  
 CC selected antigens from the same pathogen. Epitope-based anti-tumour  
 CC vaccines provides the opportunity to combine epitopes derived from  
 CC multiple tumour-associated molecules addressing the problem of tumour-  
 CC tumour variability and reducing the likelihood of tumour escape due to  
 CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
 CC the exemplification of the present invention  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 51; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VMAGVGSPPV 10  
 Db |||||  
 1 VMAGVGSPPV 10  
 RESULT 8  
 AAG88772  
 ID AAG88772 standard; peptide; 10 AA.  
 AC AAG88772;  
 XX  
 DT 11-SEP-2001 (first entry)  
 XX  
 DE HER2/neu A2 supermotif crossbinding peptide #16.  
 KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
 KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
 KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200141787-A1.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 11-DEC-2000; 2000WO-US033591.  
 XX  
 PR 11-DEC-2000; 2000WO-US033591.  
 XX

PR 10-DEC-1999; 99US-00458299.  
 XX (EPIM-) EPIMUNE INC.  
 PA Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
 PI Keogh S;  
 XX WPI; 2001-374995/39.  
 DR An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
 PT cellular immune responses for the prevention and treatment of cancer.  
 XX  
 XX Example 2; Page 179; 199pp; English.  
 XX The present invention describes isolated prepared HER2/neu epitopes (I).  
 CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
 CC culture in vitro and binds to a complex of an epitope (I), bound to a  
 CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
 CC and a second epitope and the peptide is less than 50 contiguous amino  
 CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
 CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
 CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
 CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
 CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
 CC (III) are useful for inducing cellular immune responses for the  
 CC prevention and treatment of cancer. (I) and (II) are useful for  
 CC monitoring or evaluating an immune response to a tumour-associated  
 CC antigen when incubated with a T lymphocyte sample from a patient and  
 CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
 CC based vaccines mean that immunosuppressive epitopes that may be present  
 CC in whole antigens may be avoided. Selected epitopes may be combined to  
 CC enhance immunogenicity. The possible pathological side effects caused by  
 CC infectious agents or whole protein antigen is eliminated. The vaccine  
 CC provides the ability to direct and focus an immune response to multiple  
 CC selected antigens from the same pathogen. Epitope-based anti-tumour  
 CC vaccines provides the opportunity to combine epitopes derived from  
 CC multiple tumour-associated molecules addressing the problem of tumour-  
 CC tumour variability and reducing the likelihood of tumour escape due to  
 CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
 CC the exemplification of the present invention  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 51; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VMAGVGSPPV 10  
 Db | | | | | | | | | |  
 . 1 VMAGVGSPPV 10  
 RESULT 9  
 ABB76755  
 ID ABB76755 standard; peptide; 10 AA.  
 XX  
 AC ABB76755;  
 XX  
 DT 31-MAY-2002 (first entry)  
 XX  
 DE Tumour antigen epitope HER-2/neu 773 presented by HLA A2.1.  
 XX  
 KW Antiviral; anti-HIV; cytostatic; epitope; HLA A2.1;  
 KW human leukocyte antigen; immunotherapy; cancer; viral infection; vaccine.  
 XX  
 OS Unidentified.  
 XX  
 PN FR2812087-A1.  
 XX  
 PD 25-JAN-2002.  
 XX  
 PF 21-JUL-2000; 2000FR-00009591.

PR 21-JUL-2000; 2000FR-00009591.  
 XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA Kosmatopoulos K, Tourdot S, Scardino A, Gross DA;  
 PI WPI; 2002-189846/25.  
 XX  
 DR Identifying subdominant or cryptic epitopes, useful in immunotherapy of  
 PT cancer and viral infection, comprises testing modified, non-immunogenic  
 PT peptides for induction of cytotoxic T cells.  
 XX  
 XX Example 1; Page 12; 62pp; French.  
 XX The present invention relates to subdominant/cryptic epitopes that are  
 CC presented by HLA (human leukocyte antigen) Class I molecule A2.1. The  
 CC epitopes or chimeric polypeptides containing them and nucleic acid  
 CC encoding them are useful for preventative or curative immunotherapy of  
 CC cancer and viral infections, particularly where used as vaccines. The  
 CC present peptide was used to illustrate the invention  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 51; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VMAGVGSPPV 10  
 Db | | | | | | | | | |  
 . 1 VMAGVGSPPV 10  
 RESULT 10  
 AAE26800  
 ID AAE26800 standard; peptide; 10 AA.  
 XX  
 AC AAE26800;  
 XX  
 DT 13-DEC-2002 (first entry)  
 XX  
 DE Human HLA-A2.1 restricted HER-2/neu peptide epitope #6.  
 XX  
 KW Human; cancer; breast cancer; ovarian cancer; melanoma; cell therapy;  
 KW epitope; human leukocyte antigen; HLA-A2.1.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200265992-A2.  
 XX  
 PD 29-AUG-2002.  
 XX  
 PF 19-FEB-2002; 2002WO-US005748.  
 XX  
 PR 20-FEB-2001; 2001US-0270252P.  
 XX  
 PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
 XX  
 PI Degraw J, Moriarty A, Leturcq DJ, Jackson MR, Peterson PA;  
 PI Heiskala M;  
 XX  
 DR WPI; 2002-667033/71.  
 XX  
 FT Treating a subject with cancer comprises combining the CD+8 cells, which  
 FT are stimulated with non-naturally occurring antigen-presenting cell line,  
 FT with adherent blood monocytes and inoculating the subject with CD8+  
 FT suspension.  
 XX  
 XX Example 2; Page 92; 99pp; English.  
 XX The invention relates to a method of treating a subject with cancer. The  
 CC method involves combining the CD+8 cells, which are stimulated with non  
 CC naturally occurring antigen-presenting cell (mAPC) line, with adherent  
 CC blood monocytes and inoculating the subject with CD8+ suspension. The

CC method is useful for treating cancer e.g. ovarian cancer, breast cancer  
CC and melanoma etc. It is also useful in cell therapy. The present sequence  
CC is human leukocyte antigen A2 (HLA-A2).1 restricted peptide epitope used  
CC to treat breast and ovarian cancer  
XX

XX Sequence 10 AA;

Query Match 100.0%; Score 51; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10

DB 1 VMAGVGSPPV 10

RESULT 11

AEA36306  
ID AEA36306 standard; peptide; 10 AA.

XX AEA36306;

XX 11-AUG-2005 (first entry)

XX Human HER-2/neu 773-782 cytotoxic T-lymphocyte epitope peptide.

XX viral infection; virucide; cytostatic; tumor; neoplasm; cell therapy;  
XX antigen; HER-2/neu.

XX Homo sapiens.

XX JP2005139118-A.

XX 02-JUN-2005.

XX 07-NOV-2003; 2003JP-00377653.

XX 20-FEB-2001; 2001US-0270252P.

XX (ORTH ) ORTHO-MCNEIL PHARM INC.

XX Leturco DJ, Moriarty AM, Jackson MR, Peterson PA, Richards JM;

XX WPI; 2002-667033/71.

XX Treating a subject with cancer comprises combining the CD+8 cells, which  
XX are stimulated with non-naturally occurring antigen-presenting cell line,  
XX with adherent blood monocytes and inoculating the subject with CD8+  
XX suspension.

XX Example 3; SEQ ID NO 16; 65pp; Japanese.

XX The invention relates to a novel method for treating viral infection in a  
XX subject. The method comprises preparing an antigen presentation cell  
XX lineage (mAPC), collecting CD8+ cells from the subject, stimulating CD8+  
XX cells using the mAPC, culturing CD8+ cells in the presence of  
XX interleukin-2 (IL-2) and/or IL-7, mixing peripheral blood monocytes from  
XX the subject, subjecting the components to gamma irradiation, combining  
XX the CD8+ cells with adhesive peripheral blood monocytes and inoculating  
XX the CD8+ suspended solid to the subject. The method of the invention  
XX demonstrates virucide and cytostatic activities and may be useful for  
XX treating a viral infection or tumor in a subject via cell therapy. The  
XX current sequence is that of a human HER-2/neu cytotoxic T-lymphocyte  
XX epitope peptide of the invention which was incorporated into a Drosophila  
XX antigen presenting cell.

XX Sequence 10 AA;

Query Match 100.0%; Score 51; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10

DB 1 VMAGVGSPPV 10

RESULT 12

ABU63012  
ID ABU63012 standard; peptide; 10 AA.

XX ABU63012;

XX 16-SEP-2003 (first entry)

XX Human Her-2/Neu-derived CTL epitope HER-7.

XX CTL; cytotoxic C lymphocyte; epitope; p53; cytostatic; anti-tumour;  
XX virucide; immunosuppressive; vaccine; human; immune response;  
XX tumour-associated antigen; cancer; tumour; neoplasm; viral infection;  
XX retroviral infection; autoimmune response; Her-2; Neu.

XX Homo sapiens.

XX US2003064916-A1.

XX 03-APR-2003.

XX 26-MAR-1999; 99US-00277064.

XX 08-AUG-1997; 97US-00860232.

XX (SHER/) SHERMAN L A.

XX Sherman LA;

XX WPI; 2003-512514/48.

XX Novel polypeptide useful for activating cytotoxic T lymphocytes in vivo  
XX which are useful in the diagnosis and treatment of variety of disease  
XX conditions such as cancer, tumors, and neoplasia.

XX Claim 5; Page 52; 77pp; English.

XX The invention relates to a polypeptide capable of specifically activating  
XX cytotoxic T lymphocytes (CTLs) in vivo which can then specifically target  
XX malignant cells, or having substantial homology with a CTL epitope, or  
XX its sequential subsets. Also included are a population of specific  
XX cytotoxic T cells capable of lysing tumour cells displaying a specific  
XX peptide, a vaccine comprising an immunogenically effective amount of CTL-  
XX stimulating peptide, generating activated CTL cells in vivo, generating  
XX CTL cells that will target a specific population of cells, specifically  
XX killing target cells in an individual using specific, activated CTLs,  
XX provoking an immune response to a tumour-associated antigen, identifying  
XX specific CTLs responsive to a specific T cell epitope, detecting specific  
XX CTLs having receptors capable of binding a specific T cell epitope in a  
XX tissue sample, detecting anti-p53 antibodies in an individual, an  
XX antibody molecule that immunoreacts with the polypeptide and a hybridoma  
XX capable of secreting the above antibodies. The methods are useful for  
XX specifically killing target cells in an individual using specific,  
XX activated CTLs and the polypeptide is useful for provoking an immune  
XX response to a tumour-associated antigen in mammal and the reaction occurs  
XX in vitro. The CTL epitope peptide is useful for activating CTLs in vivo  
XX with specificity for particular antigenic peptides, and these activated  
XX CTLs are useful in the diagnosis and treatment of variety of disease  
XX conditions such as cancer, tumours, neoplasia, viral and retroviral  
XX infections, and autoimmune response. The present sequence is a CTL  
XX epitope of the invention derived from the tumour associated antigen Her-  
XX 2/Neu

XX Sequence 10 AA;

Query Match 100.0%; Score 51; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVSPV 10  
 DB 1 VMAGVSPV 10  
 RESULT 13  
 ADE97756  
 ID ADE97756 standard; peptide; 10 AA.  
 AC ADE97756;  
 XX 12-FEB-2004 (first entry)  
 DT Immunogenic HLA-A2.1 binding peptide #238.  
 DE cytostatic; anti-inflammatory; hepatotropic; virucide; anti-HIV;  
 KW nephrotropic; neuroprotective; antiarthritic; antirheumatic;  
 KW immunosuppressive; dermatological; muscular; nephrotropic; thyromimetic;  
 KW haemostatic; antithyroid; antianaemic; anabolic; hypertensive;  
 KW immunogenic peptide composition; immune response; prostate cancer;  
 KW hepatitis B; hepatitis C; AIDS; renal carcinoma; cervical carcinoma;  
 KW lymphoma; cytomegalovirus; CMV; condyloma acuminatum;  
 KW autoimmune associated disorder; multiple sclerosis; rheumatoid arthritis;  
 KW Sjogren syndrome; scleroderma; polymyositis; dermatomyositis;  
 KW systemic lupus erythematosus; juvenile rheumatoid arthritis;  
 KW ankylosing spondylitis; myasthenia gravis; MG; bullous pemphigoid;  
 KW pemphigus; glomerulonephritis; Goodpasture's syndrome;  
 KW autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia;  
 KW idiopathic thrombocytopenic purpura; Grave's disease; Addison's disease;  
 KW human leukocyte antigen A2.1; HLA A2.1;  
 KW immunogenic HLA-A2.1 binding peptide.  
 OS Synthetic.  
 XX US2003185822-A1. - cannot be used as 102(e) bec.  
 XX 02-OCT-2003.  
 XX 03-APR-2002; 2002US-00116557.  
 XX 05-MAR-1993; 93US-00027146.  
 XX 04-JUN-1993; 93US-00073205.  
 XX 29-NOV-1993; 93US-00159184.  
 XX 02-DEC-1994; 94US-00349177.  
 XX (GREY/) GREY H M.  
 XX (SETT/) SETTE A.  
 XX (SIDN/) SIDNEY J.  
 XX Grey HM, Sette A, Sidney J;  
 XX WPI; 2004-041186/04.  
 XX Immunogenic peptide composition for preventing, treating or diagnosing  
 PT pathological states, e.g. prostate cancer, hepatitis B and C, Acquired  
 PT Immunodeficiency Syndrome, and renal carcinoma, includes conserved  
 PT residues at specified positions.  
 XX Example 11; Page 25; 38pp; English.  
 XX The invention describes an immunogenic peptide composition comprising 9  
 CC residues including a first conserved residue at a second position from N-  
 CC terminus, and a second conserved residue at C-terminal position. The  
 CC inventive peptide composition is used to elicit an immune response  
 CC against a desired antigen for preventing, treating or diagnosing  
 CC pathological states, e.g. prostate cancer, hepatitis B, hepatitis C,  
 CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, cytomegalovirus  
 CC (CMV), and condyloma acuminatum. It is also used to treat autoimmune  
 CC associated disorders, e.g. multiple sclerosis, rheumatoid arthritis,  
 CC Sjogren syndrome, scleroderma, polymyositis, dermatomyositis, systemic  
 CC lupus erythematosus, juvenile rheumatoid arthritis, ankylosing  
 CC spondylitis, myasthenia gravis (MG), bullous pemphigoid, pemphigus,  
 CC glomerulonephritis, Goodpasture's syndrome, autoimmune hemolytic anemia,

CC Hashimoto's disease, pernicious anaemia, idiopathic thrombocytopenic  
 CC purpura, Grave's disease, and Addison's disease. The invention defines  
 CC positions within a motif enabling the selection of the peptides, which  
 CC will bind efficiently to human leukocyte antigen (HLA) A2.1. This is the  
 CC amino acid sequence of an immunogenic HLA-A2.1 binding peptide.  
 XX Sequence 10 AA;  
 SQ Query Match 100.0%; Score 51; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VMAGVSPV 10  
 DB 1 VMAGVSPV 10  
 RESULT 14  
 ADM12647  
 ID ADM12647 standard; peptide; 10 AA.  
 XX ADM12647;  
 AC ADM12647;  
 XX 20-MAY-2004 (first entry)  
 DT MHC class I epitope of human Her-2/neu, 16-6-9.  
 DE antigen presentation enhancing hybrid polypeptide; mammalian II-Key;  
 KW MHC class II; antibacterial; virucide; fungicide; antirheumatic;  
 KW antiarthritic; neuroprotective; dermatological; immunosuppressive;  
 KW antiinflammatory; antidiabetic; antithyroid; immune;  
 KW rheumatoid arthritis; multiple sclerosis; lupus erythematosus;  
 KW diabetes mellitus; myasthenia gravis; autoimmune thyroiditis;  
 KW scleroderma; dermatomyositis; pemphigus.  
 OS Homo sapiens.  
 XX US2003235594-A1.  
 XX 25-DEC-2003.  
 XX 17-SEP-2002; 2002US-00245871.  
 XX 14-SEP-1999; 99US-00396813.  
 XX 17-JUL-2002; 2002US-00197000.  
 XX (ANTI-) ANTIGEN EXPRESS INC.  
 XX Humphreys R, Xu M;  
 XX WPI; 2004-070554/07.  
 XX Novel II-Key/antigen presentation enhancing hybrid polypeptide, useful  
 PT for treating infections, rheumatoid arthritis, multiple sclerosis, lupus  
 PT erythematosus and diabetes mellitus.  
 XX Example 16; Page 55; 87pp; English.  
 XX The invention relates to a novel antigen presentation enhancing hybrid  
 CC polypeptide. The novel polypeptide has an N-terminal element consisting  
 CC of 4-16 residues of a mammalian II-Key peptide and its non-N-terminal  
 CC deletion modifications, a chemical structure covalently linking the N-  
 CC terminal element to an MHC class II-presented epitope of a C-terminal  
 CC element. The C-terminal element comprises an antigenic epitope, which  
 CC binds to an antigenic peptide binding site of an MHC class II molecule.  
 CC The antigen presentation enhancing hybrid polypeptide has the following  
 CC activities: antibacterial, virucide, fungicide, antirheumatic,  
 CC antiarthritic, neuroprotective, dermatological, immunosuppressive,  
 CC antiinflammatory, antidiabetic, and antithyroid. The antigen presentation  
 CC enhancing hybrid polypeptide is useful for modulating the immune response  
 CC in an individual and for treating infections (such as bacteria, virus,  
 CC parasite and fungus), rheumatoid arthritis, multiple sclerosis, lupus  
 CC erythematosus, diabetes mellitus, myasthenia gravis, autoimmune

of the file date of 03/26/99  
 the application

CC thyroiditis, scleroderma, dermatomyositis and pemphigus. This sequence  
 CC represents a mammalian II key related peptide epitope of the invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 51; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VMAGVGSPV 10  
 DB 1 VMAGVGSPV 10  
 |||||  
 |||||  
 RESULT 15  
 ADO38880  
 ID ADO38880 standard; peptide; 10 AA.  
 XX  
 AC ADO38880;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Human Her-2/neu MHC class II-presented epitope #67.  
 KW Antibacterial; Virucide; Fungicide; Antiparasitic; Antiarthritic;  
 KW Antirheumatic; Neuroprotective; Antiinflammatory; Dermatological;  
 KW Immunosuppressive; Antidiabetic; Antithyroid; Antiallergic;  
 KW Antiallergic; Cytostatic; Antiproliferative; Gene Therapy; Vaccine;  
 KW MHC Class II; II-key motif; immune response; anthrax; EBOLA; HIV;  
 KW influenza; vaccinia virus; infection; bacterium; virus; parasite; fungus;  
 KW rickettsia; rheumatoid arthritis; multiple sclerosis;  
 KW lupus erythematosus; diabetes mellitus; myasthenia gravis;  
 KW autoimmune thyroiditis; scleroderma; dermatomyositis; pemphigus; asthma;  
 KW allergic rhinitis; topical dermatitis; colitis; cancer; psoriasis;  
 KW adenoma.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2004058881-A1.  
 XX  
 PD 25-MAR-2004.  
 XX  
 PP 24-SEP-2002; 2002US-00253286.  
 XX  
 PR 24-SEP-2002; 2002US-00253286.  
 XX  
 PA (ANTI-) ANTIGEN EXPRESS INC.  
 XX  
 PI Humphreys RE, Xu M;  
 XX  
 DR WPI; 2004-294259/27.  
 XX  
 PT New non-naturally occurring protein or polypeptide modified by  
 PT recombinant DNA techniques, useful for treating multiple sclerosis,  
 PT diabetes mellitus, myasthenia gravis, scleroderma, allergic rhinitis,  
 PT colitis, cancer or psoriasis.  
 XX  
 PS Example 16; Page 57; 90pp; English.  
 XX  
 CC The invention relates to a non-naturally occurring protein or polypeptide  
 CC (I) modified by recombinant DNA techniques comprising: a C-terminal  
 CC element comprising an MHC Class II-presented epitope; an N-terminal  
 CC element comprising an II-key motif; and an intervening element comprising  
 CC a sequence of 4-11 amino acid residues where the modification by  
 CC recombinant DNA techniques taking place within elements (b) and (c). Also  
 CC described are methods for: suppressing or enhancing an immune response  
 CC directed toward an MHC (major histocompatibility complex) Class II-  
 CC presented epitope of interest. Suppressing an immune response directed  
 CC toward an MHC Class II-presented epitope of interest comprises: providing  
 CC a nucleic acid sequence encoding the MHC Class II-presented epitope of  
 CC interest, the nucleic acid sequence encoding an II-key motif located 4-11  
 CC amino acids upstream from the N-terminal residue of the MHC Class II-  
 CC presented epitope of interest; and modifying the II-key motif to decrease

CC its conformance to the archetypal II-key regulatory motif. Enhancing an  
 CC immune response directed toward an MHC Class II-presented epitope of  
 CC interest comprises: providing a nucleic acid sequence encoding the MHC  
 CC Class II-presented epitope of interest, the nucleic acid sequence lacking  
 CC an II-key motif located 4-11 amino acids upstream from the N-terminal  
 CC residue of the MHC Class II-presented epitope of interest; and modifying  
 CC the nucleic acid sequence to introduce an II-key motif appropriately  
 CC spaced from the MHC Class II-presented epitope. The protein or  
 CC polypeptide of interest corresponds to a protein or polypeptide encoded  
 CC by an infectious pathogen selected from anthrax, EBOLA, HIV or influenza,  
 CC preferably vaccinia virus. The non-natural DNA techniques is useful for  
 CC polypeptide (I) modified by recombinant DNA techniques is useful for  
 CC treating infectious diseases caused or associated with infection by a  
 CC bacterium, virus, parasite, fungus, rickettsia or other infectious  
 CC agents. It is also useful for treating rheumatoid arthritis, multiple  
 CC sclerosis, lupus erythematosus, diabetes mellitus, myasthenia gravis,  
 CC autoimmune thyroiditis, scleroderma, dermatomyositis, pemphigus, asthma,  
 CC allergic rhinitis, topical dermatitis, colitis, cancer, psoriasis or  
 CC adenomas. The present sequence represents the amino acid sequence of an  
 CC MHC class II-presented epitope used in the invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 51; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VMAGVGSPV 10  
 DB 1 VMAGVGSPV 10  
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 Job time : 190 secs

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OM protein - protein search, using sw model

Run on: April 11, 2006, 19:24:25 : Search time 24 Seconds  
(without alignments)  
12.997 Million cell updates/sec

Title: US-09-277-064-12

Perfect score: 51

Sequence: 1 VMAGVGSPPV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 48921

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:\*

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- 2: /SIDSS/prodata/1/pubpaa/US06\_NEW\_PUB.pap:\*
- 3: /SIDSS/prodata/1/pubpaa/US07\_NEW\_PUB.pap:\*
- 4: /SIDSS/prodata/1/pubpaa/US09\_NEW\_PUB.pap:\*
- 5: /SIDSS/prodata/1/pubpaa/US09\_NEW\_PUB.pap:\*
- 6: /SIDSS/prodata/1/pubpaa/US10\_NEW\_PUB.pap:\*
- 7: /SIDSS/prodata/1/pubpaa/US11\_NEW\_PUB.pap:\*
- 8: /SIDSS/prodata/1/pubpaa/US16\_NEW\_PUB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	7	US-11-033-039-620
2	41	80.4	9	6	US-10-510-101-135
3	29	56.9	9	7	US-11-045-024-2492
4	29	56.9	9	7	US-11-045-024-7995
5	29	56.9	10	7	US-11-045-024-2498
6	29	56.9	10	7	US-11-045-024-4891
7	29	56.9	10	7	US-11-045-024-6819
8	26	51.0	9	6	US-10-966-483-5
9	26	51.0	9	6	US-10-511-273-7
10	24	47.1	9	6	US-10-517-784-42
11	24	47.1	10	7	US-11-125-837-12
12	23	45.1	8	7	US-11-045-024-2949
13	23	45.1	8	7	US-11-045-024-2950
14	23	45.1	8	7	US-11-045-024-9135
15	23	45.1	8	7	US-11-045-024-9136
16	23	45.1	8	7	US-11-045-024-9240
17	23	45.1	8	7	US-11-045-024-9252
18	23	45.1	8	7	US-11-045-024-11312
19	23	45.1	8	7	US-11-045-024-11313
20	23	45.1	8	7	US-11-045-024-11376
21	23	45.1	8	7	US-11-045-024-11383
22	23	45.1	9	7	US-11-021-441-67
23	23	45.1	9	7	US-11-045-024-1234
24	23	45.1	9	7	US-11-045-024-1235
25	23	45.1	9	7	US-11-045-024-9139

26	23	45.1	9	7	US-11-045-024-9140	Sequence 9140, Ap
27	23	45.1	9	7	US-11-045-024-9242	Sequence 9242, Ap
28	23	45.1	9	7	US-11-045-024-9255	Sequence 9255, Ap
29	23	45.1	9	7	US-11-045-024-11315	Sequence 11315, A
30	23	45.1	9	7	US-11-045-024-11377	Sequence 11377, A
31	23	45.1	9	7	US-11-033-039-467	Sequence 467, App
32	23	45.1	10	7	US-11-045-024-3016	Sequence 3016, Ap
33	23	45.1	10	7	US-11-045-024-3017	Sequence 3017, Ap
34	23	45.1	10	7	US-11-045-024-9127	Sequence 9127, Ap
35	23	45.1	10	7	US-11-045-024-9142	Sequence 9142, Ap
36	23	45.1	10	7	US-11-045-024-9143	Sequence 9143, Ap
37	23	45.1	10	7	US-11-045-024-9244	Sequence 9244, Ap
38	23	45.1	10	7	US-11-045-024-9245	Sequence 9245, Ap
39	23	45.1	10	7	US-11-045-024-9257	Sequence 9257, Ap
40	23	45.1	10	7	US-11-045-024-11306	Sequence 11306, A
41	23	45.1	10	7	US-11-045-024-11317	Sequence 11317, A
42	23	45.1	10	7	US-11-045-024-11378	Sequence 11378, A
43	23	45.1	10	7	US-11-045-024-11386	Sequence 11386, A
44	22	43.1	6	7	US-11-032-773-743	Sequence 743, App
45	22	43.1	6	7	US-11-197-315-6	Sequence 6, Appl

#### ALIGNMENTS

RESULT 1  
US-11-033-039-620  
; Sequence 620, Application US/11033039  
; Publication No. US20060002947A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; CURRENT APPLICATION NUMBER: US/11/033,039  
; CURRENT FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: 10/245,871  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 1452  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 620  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-033-039-620

Query Match 100.0%; Score 51; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00065;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VMAGVGSPPV 10  
Db 1 VMAGVGSPPV 10

RESULT 2  
US-10-510-101-135  
; Sequence 135, Application US/10510101  
; Publication No. US20060018915A1  
; GENERAL INFORMATION:  
; APPLICANT: Epiimmune Inc.  
; APPLICANT: Iehioka, Glenn  
; APPLICANT: Fikes, John  
; APPLICANT: Tangri, Shabnam  
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods  
; FILE REFERENCE: 2060.009PC05  
; CURRENT APPLICATION NUMBER: US/10/510,101  
; CURRENT FILING DATE: 2004-10-05

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; PRIOR APPLICATION NUMBER: US 60/413,471
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 10/116,118
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 135
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide derived from Homo sapiens Her2/neu
US-10-510-101-135

Query Match      80.4%; Score 41; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VMAGVGSPI 9
Db 1 VMDGVGSPI 9

RESULT 3
US-11-045-024-2492
; Sequence 2492, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2492
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2492

Query Match      56.9%; Score 29; DB 7; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.4e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GVGSPYV 10
Db 3 GVGSPQI 9

RESULT 5
US-11-045-024-2498
; Sequence 2498, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2492
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2498

Query Match      56.9%; Score 29; DB 7; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.4e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GVGSPYV 10
Db 3 GVGSPQI 9

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Db 3 GVGSPQI 9

RESULT 4
US-11-045-024-7995
; Sequence 7995, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7995
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-7995

Query Match      56.9%; Score 29; DB 7; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.4e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GVGSPYV 10
Db 3 GVGSPQI 9

RESULT 5
US-11-045-024-2498
; Sequence 2498, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
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; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2498
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2498

Query Match      56.9%; Score 29; DB 7; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.4e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GVGSPYV 10
Db 3 GVGSPQI 9

```

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; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2498
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2498

Query Match      56.9%; Score 29; DB 7; Length 10;
Best Local Similarity 71.4%; Pred. No. 10;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 GVGSPYV 10
Db      4 GVGSPQI 10

RESULT 6
US-11-045-024-4891
; Sequence 4891, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Cheenut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6819
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6819

Query Match      56.9%; Score 29; DB 7; Length 10;
Best Local Similarity 71.4%; Pred. No. 10;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 GVGSPYV 10
Db      4 GVGSPQI 10

RESULT 7
US-11-045-024-6819
; Sequence 6819, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Cheenut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6819
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6819

Query Match      56.9%; Score 29; DB 7; Length 10;
Best Local Similarity 71.4%; Pred. No. 10;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 GVGSPYV 10
Db      4 GVGSPQI 10

RESULT 8
US-10-966-483-5
; Sequence 5, Application US/10966483
; Publication No. US20050281783A1
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```

; GENERAL INFORMATION:
; APPLICANT: Kinch, Michael S.
; APPLICANT: Kiener, Peter A.
; APPLICANT: Bruckheimer, Elizabeth
; APPLICANT: Dubensky, Jr. Thomas W.
; APPLICANT: Cook, David N.
; TITLE OF INVENTION: LISTERIA-BASED EPHA2 VACCINES
; FILE REFERENCE: 10271-146
; CURRENT APPLICATION NUMBER: US/10/966,483
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/511,919
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 60/511,719
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 60/532,666
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/556,631
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE: 2004-10-07
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-483-5

Query Match 51.0%; Score 26; DB 6; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAVG 6
Db 1 VLAGVG 6

RESULT 9
US-10-511-273-7
; Sequence 7, Application US/10511273
; Publication No. US20060034856A1
; GENERAL INFORMATION:
; APPLICANT: ALVES, PEDRO
; APPLICANT: KOSMATOPOULOS, KOSTAS
; TITLE OF INVENTION: EPHA2 ANTIGEN T EPITOPES
; FILE REFERENCE: 260449USXPCT
; CURRENT APPLICATION NUMBER: US/10/511,273
; CURRENT FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: PCT/FR03/01280
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: FR 02/05048
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-511-273-7

Query Match 51.0%; Score 26; DB 6; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAVG 6
Db 1 VLAGVG 6

RESULT 10
US-10-517-784-42
; Sequence 42, Application US/10517784
; Publication No. US20060003315A1
; GENERAL INFORMATION:
; APPLICANT: GROSS, Gideon
; APPLICANT: MARGALIT, Alon
; TITLE OF INVENTION: MEMBRANE-ANCHORED BETA-2 MICROGLOBULIN COVALENTLY LINKED TO MHC
; TITLE OF INVENTION: PEPTIDE EPITOPES
; FILE REFERENCE: GAVISH-004 US
; CURRENT APPLICATION NUMBER: US/10/517,784
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 60/388,273
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/IL03/00501
; PRIOR FILING DATE: 2003-06-12
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-517-784-42

Query Match 47.1%; Score 24; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 MAGVSPY 9
Db 1 LLGPGRPY 8

RESULT 11
US-11-125-837-12
; Sequence 12, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-12

Query Match 47.1%; Score 24; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GSPY 9
Db 2 GSPY 5

RESULT 12
US-11-045-024-2949
; Sequence 2949, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
```



Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GVGSP 8  
|||  
Db 2 GVGSP 6

RESULT 15  
US-11-045-024-9136  
; Sequence 9136, Application US/11045024  
; Publication No. US20050271676A1  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Baker, Denise Marie  
; APPLICANT: Celis, Esteban  
; APPLICANT: Kubo, Ralph  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
; FILE REFERENCE: 2060.0040007  
; CURRENT APPLICATION NUMBER: US/11/045,024  
; CURRENT FILING DATE: 2005-01-28  
; PRIOR APPLICATION NUMBER: US 09/412,863  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: US 08/027,146  
; PRIOR FILING DATE: 1993-03-05  
; PRIOR APPLICATION NUMBER: US 08/073,205  
; PRIOR FILING DATE: 1993-06-04  
; PRIOR APPLICATION NUMBER: US 08/103,396  
; PRIOR FILING DATE: 1993-08-06  
; PRIOR APPLICATION NUMBER: US 08/159,184  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/159,339  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/205,713  
; PRIOR FILING DATE: 1994-03-04  
; PRIOR APPLICATION NUMBER: US 08/347,610  
; PRIOR FILING DATE: 1994-12-01  
; NUMBER OF SEQ ID NOS: 14528  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9136  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-9136

Query Match 45.1%; Score 23; DB 7; Length 8;  
Best Local Similarity 80.0%; Pred. No. 1.4e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GVGSP 8  
|||  
Db 1 GVGSP 5

Search completed: April 11, 2006, 19:27:28  
Job time : 25 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2006, 19:18:59 ; Search time 38 Seconds  
(without alignments)  
25.320 Million cell updates/sec

Title: US-09-277-064-12

Perfect score: 51

Sequence: 1 VMAGVGSFYV 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	47.1	9	2 PH1591	Ig H chain V-D-J r
2	19	37.3	8	2 E47393	neuropeptide calla
3	18	35.3	7	2 T09512	NADH2 dehydrogenas
4	18	35.3	8	2 F60588	sperm-activating p
5	18	35.3	9	2 S65865	collagen alpha 2(V
6	17	33.3	5	2 A41235	copper resistance
7	17	33.3	6	2 A27696	contraction-inhibi
8	17	33.3	8	2 PT0627	T-cell receptor be
9	17	33.3	9	2 PT0324	Ig heavy chain CRD
10	17	33.3	10	2 C39111	Ig heavy chain C r
11	17	33.3	10	2 G60787	sperm-activating p
12	17	33.3	10	2 I60588	sperm-activating p
13	16	31.4	5	2 C3751	spinal cord peptid
14	16	31.4	7	2 PT0623	T-cell receptor be
15	16	31.4	8	2 PT0631	T-cell receptor be
16	16	31.4	8	2 G60588	sperm-activating p
17	16	31.4	10	2 PT0210	Ig heavy chain CDR
18	16	31.4	10	2 PH0927	T-cell receptor be
19	16	31.4	10	2 H60787	sperm-activating p
20	16	31.4	10	2 F60787	sperm-activating p
21	16	31.4	10	2 D60787	sperm-activating p
22	16	31.4	10	2 B60787	sperm-activating p
23	16	31.4	10	2 D60588	sperm-activating p
24	16	31.4	10	2 C60588	sperm-activating p
25	16	31.4	10	2 I60527	sperm-activating p
26	16	31.4	10	2 I60527	sperm-activating p
27	16	31.4	10	2 D60527	sperm-activating p
28	16	31.4	10	2 C39572	sperm-activating p
29	16	31.4	10	2 F60527	sperm-activating p

30 16 31.4 10 2 C60527 sperm-activating p  
31 16 31.4 10 2 E60527 sperm-activating p  
32 16 31.4 10 2 G60527 sperm-activating p  
33 16 31.4 10 2 E39572 sperm-activating p  
34 16 31.4 10 2 D60788 sperm-activating p  
35 16 31.4 10 2 E60788 sperm-activating p  
36 16 31.4 10 2 C60788 sperm-activating p  
37 16 31.4 10 2 F60589 sperm-activating p  
38 16 31.4 10 2 C60589 sperm-activating p  
39 16 31.4 10 2 D60589 sperm-activating p  
40 16 31.4 10 2 A60527 sperm-activating p  
41 16 31.4 10 2 A60787 sperm-activating p  
42 16 31.4 10 2 A60588 sperm-activating p  
43 16 31.4 10 2 A60788 sperm-activating p  
44 15 29.4 5 2 I40702 primase - Citrobac  
45 15 29.4 6 2 I51434 H4 histone - Afric

#### ALIGNMENTS

##### RESULT 1

PH1591  
Ig H chain V-D-J region (wild-type clone 142) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C/Accession: PH1591  
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic  
A/Reference number: PH1580; MUID:93301609; PMID:8315387.  
A/Accession: PH1591  
A/Molecule type: DNA  
A/Residues: 1-9 <LEV>  
A/Cross-references: UNIPARC:UPI000017C6B2  
A/Experimental source: bone marrow pre-B lymphocyte  
C/Keywords: immunoglobulin

Query Match 47.1%; Score 24; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GSPY 9

Db 4 GSPY 7

##### RESULT 2

E47393  
neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria)  
C/Species: Calliphora vomitoria  
C/Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: E47393  
R/Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.  
Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993  
A/Title: Callatostatin: neuropeptides from the blowfly Calliphora vomitoria with sequ  
A/Reference number: A47393; MUID:93211980; PMID:8460157  
A/Accession: E47393  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-8 <DUV>

A/Cross-references: UNIPROT:P41841; UNIPARC:UPI000002EAB5  
A/Experimental source: whole flies  
A/Note: sequence extracted from NCBI backbone (NCBIP:128482)

Query Match 37.3%; Score 19; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GSPY 9

Db 1 GPPY 4



A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 33.3%; Score 17; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGVG 6  
|||  
Db 5 AGLG 8

## RESULT 9

PT0324  
IG heavy chain CRD3 region (clone J2-106C) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0324  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0324  
A;Molecule type: DNA  
A;Residues: 1-9 <YAM>  
A;Cross-references: UNIPARC:UPI000017C217  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 17; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GVGSPY 9  
|||  
Db 3 GYGESY 8

## RESULT 10

C39111  
Ig heavy chain C region - Pacific hagfish (fragment)  
C;Species: Eptatretus stoutii (Pacific hagfish)  
C;Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 16-Aug-1996  
C;Accession: C39111  
R;Varner, J.; Neame, P.; Litman, G.W.  
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991  
A;Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simil  
A;Reference number: A39111; MUID:91156684; PMID:2000382  
A;Accession: C39111  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <VAR>  
A;Cross-references: UNIPARC:UPI000017BP2B  
C;Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 17; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 4.9e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 VGSPVY 10  
|||  
Db 4 ISSPLV 9

## RESULT 11

G60787  
sperm-activating peptide (Ser-3,5,7 speract) - sea urchin (Anthocidaris crassispina)  
C;Species: Anthocidaris crassispina  
C;Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 16-Aug-2004  
C;Accession: G60787  
R;Suzuki, N.; Kajitara, H.; Nomura, K.; Garbets, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.  
Comp. Biochem. Physiol. B 89, 687-693, 1988  
A;Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentro

A;Reference number: A60787; MUID:88242184; PMID:3378407

A;Accession: G60787  
A;Molecule type: protein  
A;Residues: 1-10 <SUZ>  
A;Cross-references: UNIPROT:Q7M4D8; UNIPARC:UPI000017A4D6  
C;Comment: This oligopeptide from egg jelly, is one of several from this species, all of  
at shows some, but not absolute, species restriction.

Query Match 33.3%; Score 17; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 4.9e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGVG 6  
|||  
Db 7 SGVG 10

## RESULT 12

I60588  
sperm-activating peptide (Glu-3, Met-4, Gly-5, Thr-7 SAP-I) - slate-pencil urchin (Heter  
C;Species: Heterocentrotus mamillatus  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-2004  
C;Accession: I60588  
R;Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamag  
Comp. Biochem. Physiol. B 94, 739-751, 1989  
A;Title: A halogenated amino acid-containing sperm activating peptide and its related f  
otus nudus, Echinometra mathaei and Heterocentrotus mamillatus.  
A;Reference number: A60527  
A;Accession: I60588  
A;Molecule type: protein  
A;Residues: 1-10 <YOS>  
A;Cross-references: UNIPROT:Q7M4C0; UNIPARC:UPI000017A4EB

Query Match 33.3%; Score 17; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 4.9e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 MAGVG 6  
|||  
Db 4 MGGTG 8

## RESULT 13

C23751  
spinal cord peptide SCP-6 - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 28-Sep-1987 #sequence\_revision 28-Sep-1987 #text\_change 16-Aug-2004  
C;Accession: C23751  
R;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou,  
Arch. Biochem. Biophys. 240, 178-183, 1985  
A;Reference number: A23751; MUID:85250425; PMID:4015098  
A;Accession: C23751  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <HSI>  
A;Cross-references: UNIPARC:UPI000017A4FA

Query Match 31.4%; Score 16; DB 2; Length 5;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGVG 6  
|||  
Db 2 AGAG 5

## RESULT 14

PT0623  
T-cell receptor beta chain V-D-J region (111-1AB) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0623  
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0623  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-7 <FEE>  
A;Cross-references: UNIPARC:UPI000017C7CB  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 31.4%; Score 16; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGVG 6  
|||  
Db 4 AGTG 7

## RESULT 15

PT0631  
T-cell receptor beta chain V-D-J region (111-11) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0631  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0631  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-8 <FEE>  
A;Cross-references: UNIPARC:UPI000017C7D4  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 31.4%; Score 16; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGVG 6  
|||  
Db 5 AGTG 8

Search completed: April 11, 2006, 19:23:18  
Job time : 39 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 11, 2006, 19:15:49 ; Search time 229 Seconds  
(without alignments)  
30.809 Million cell updates/sec

Title: US-09-277-064-12

Perfect score: 51

Sequence: 1 VMAGVGSPV 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 3063

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	47.1	8	Q8GTG5 LYCES	Q8GTG5 lycopersico
2	20	39.2	8	ALL16_CARMA	P81819 carcinus ma
3	20	39.2	8	ALL16_CARMA	P81812 carcinus ma
4	19	37.3	8	ALL15_CALVO	P41841 calliphora
5	19	37.3	9	Q6LDB5 HUMAN	Q6LDB5 homo sapien
6	19	37.3	9	Q9UQW0 HUMAN	Q9UQW0 homo sapien
7	19	37.3	10	Q67B09 CAUD	Q67B09 bacterioph
8	19	37.3	10	Q76MK9 STELE	Q76MK9 eurypharynx
9	19	37.3	10	Q76MM5 STELE	Q76MM5 eurypharynx
10	18	35.3	7	Q07624 9RETR	Q07624 rous sarcom
11	18	35.3	8	ALL7_CARMA	P81809 carcinus ma
12	18	35.3	10	FAR6_PANRE	P82660 panagrellus
13	18	35.3	10	Q7SA22 NEUCR	Q7SA22 neurospora
14	18	35.3	10	Q6OHF3 9LABR	Q6OHF3 xyrichtys d
15	17	33.3	6	C1PI MYTED	P13736 mytilus edu
16	17	33.3	7	FAR1 HELTI	P41871 helisoma tr
17	17	33.3	8	DYS1 LIMIN	P82079 limnodynast
18	17	33.3	8	Q5ZEY7 HUMAN	Q5ZEY7 homo sapien
19	17	33.3	8	Q9R772 ECOLI	Q9R772 escherichia
20	17	33.3	9	Q4YF00 PLABE	Q4YF00 plasmodium
21	17	33.3	9	Q811S2 MOUSE	Q811S2 mus musculu
22	17	33.3	10	RT02 BOVIN	P82923 bos taurus
23	17	33.3	10	TKU2 UREUN	P40752 urechis uni
24	17	33.3	10	Q7M4C0 HETMA	Q7M4C0 heterocentr
25	17	33.3	10	QAX386 FLACH	QAX386 plasmodium
26	17	33.3	10	Q7M4D8 ANTCH	Q7M4D8 anthocidari
27	17	33.3	10	Q6OHF1 9LABR	Q6OHF1 cheilio ine
28	17	33.3	10	Q9PRY8 TRISC	Q9PRY8 triakis scy
29	16	31.4	7	Q9BRV4 HUMAN	Q9BRV4 homo sapien
30	16	31.4	7	Q8KM33 9ENTR	Q8KM33 klebsiella
31	16	31.4	8	CAD1_ENTIFA	P13269 enterococcu

32	16	31.4	8	1	VGLG_HHV2B	P81780 human herpe
33	16	31.4	8	2	Q7M4C6_PSEMC	Q7M4C6 pseudobolat
34	16	31.4	8	2	Q9GMH3_LAGOB	Q9GMH3 lagenorhync
35	16	31.4	9	2	Q7RA82_PLAYO	Q7RA82 plasmodium
36	16	31.4	9	2	Q7JIS3_LAGOB	Q7JIS3 lagenorhync
37	16	31.4	9	2	Q7JIS4_LAGOL	Q7JIS4 lagenorhync
38	16	31.4	9	2	Q7JIS5_LAGOL	Q7JIS5 lagenorhync
39	16	31.4	9	2	Q7JIS6_LAGOL	Q7JIS6 lagenorhync
40	16	31.4	9	2	Q7JIS7_LAGOL	Q7JIS7 lagenorhync
41	16	31.4	9	2	Q7JIS8_LAGOL	Q7JIS8 lagenorhync
42	16	31.4	9	2	Q7JIS9_LAGAC	Q7JIS9 lagenorhync
43	16	31.4	9	2	Q7JIT0_LAGAC	Q7JIT0 lagenorhync
44	16	31.4	9	2	Q7JIT1_LAGAC	Q7JIT1 lagenorhync
45	16	31.4	9	2	Q9GJVI_LAGAC	Q9GJVI lagenorhync

#### ALIGNMENTS

RESULT 1  
Q8GTG5 LYCES PRELIMINARY; PRT; 8 AA.  
ID Q8GTG5;  
AC Q8GTG5;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE WRKY transcription factor Iid-1 splice variant 2 (fragment).  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.  
ON NCBI\_TaxID=4081;  
RX [1]  
RN NUCLEOTIDE SEQUENCE.  
RP TISSUE=Young leaves;  
RA Cagna G., Boes A., Ulker B., Zhou A., Wanke D., Somssich I.E.;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY157059; AA71729.1; -; mRNA.  
FT NON TER 1  
SQ SEQUENCE 8 AA; 917 MW; 59177B4775B87330 CRC64;

Query Match 47.1%; Score 24; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GSPY 9  
Db 3 GSPY 6

RESULT 2  
ALL16\_CARMA STANDARD; PRT; 8 AA.  
ID ALL16\_CARMA  
AC P81813;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Carcinus maenas (Common shore crab) (Green crab).  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Decapoda; Decapoda; Pleocyemata; Brachyura;  
OC Brachyura; Portunoidae; Portunidae; Carcinus.  
ON NCBI\_TaxID=6759;  
RX [1]  
RN PROTEIN SEQUENCE.  
RP TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestros J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
allatostatin superfamily in the shore crab Carcinus maenas";  
RL Eur. J. Biochem. 250:727-734 (1997).  
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.

```
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the allatostatin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Annotation: Direct protein sequencing; Multigene family; Neuropeptide.
KW MOD RES 8 8 Leucine amide.
SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;

Query Match 39.2%; Score 20; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GSPY 9
DB 1 GGPY 4

RESULT 3
ALL5_CALVO STANDARD; PRT; 8 AA.
AC P81812;
DT 30-MAY-2000 (Rel. 39, Created)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Carcinustatin-9.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734 (1997).
CC -|- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the allatostatin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Annotation: Direct protein sequencing; Multigene family; Neuropeptide.
KW MOD RES 8 8 Leucine amide.
SQ SEQUENCE 8 AA; 781 MW; 7C2879CDB476878 CRC64;

Query Match 39.2%; Score 20; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GSPY 9
DB 1 GGPY 4

RESULT 4
ALL5_CALVO STANDARD; PRT; 8 AA.
AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
```

```
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Callatostatin-5 (Met-callatostatin-1) ([Hyp3]Met-callatostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroides;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93211390; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatin.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460 (1993).
RN [2]
RC CHARACTERIZATION, AND HYDROXYLATION.
RX TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-callatostatin. Identification and biological properties of
RT a novel neuropeptide from the blowfly Calliphora vomitoria.";
RL J. Biol. Chem. 269:21059-21066 (1994).
CC -|- FUNCTION: May act as a neurotransmitter or neuromodulator and play
CC a role in the integration of information within the brain. May be
CC involved in the control of visceral muscles due to its ability to
CC behave as potent inhibitors of peristaltic movements. May also
CC fulfill a neurohormonal role on muscles of the gut and heart.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Neurons within brain and abdominal ganglion.
CC -|- SIMILARITY: Belongs to the allatostatin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; E47393; E47393.
KW Amidation; Direct protein sequencing; Hydroxylation; Neuropeptide.
FT MOD RES 3 3 Hydroxyproline (partial).
FT MOD RES 8 8 Methionine amide.
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;

Query Match 37.3%; Score 19; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GSPY 9
DB 1 GGPY 4

RESULT 5
O6LDB5_HUMAN PRELIMINARY; PRT; 9 AA.
AC O6LDB5;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Lamp-2 protein (Fragment).
GN Name=lamp-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93286154; PubMed=8509432;
RA Sawada R., Jardine K.A., Fukuda M.;
RT "The genes of major lysosomal membrane glycoproteins lamp-1 and lamp-
RT 2. The 5'-flanking sequence of lamp-2 gene and comparison of exon
```

```
RT organization in two genes.";
RL J. Biol. Chem. 268:13010-13010(1993).
DR EMBL; S62577; AAR27101.1; -; Genomic_DNA.
FT NON TER 9
SQ SEQUENCE 9 AA; 995 MW; 8C8EA5B877376DDA CRC64;

Query Match 37.3%; Score 19; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2.2e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGVGSPY 9
|:|:|
Db 3 APLGSSY 9

RESULT 6
Q9UQW0 HUMAN PRELIMINARY; PRT; 9 AA.
AC Q9UQW0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Prolactin precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84182507; PubMed=6325171;
RA Truong A.T., Duez C., Belayew A., Renard A., Pictet R.L., Bell G.I.,
RA Martial J.A.;
RT "Isolation and characterization of the human prolactin gene.";
RL EMBO J. 3:429-437(1984).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93076813; PubMed=1332868;
RA Peers B., Naida A.M., Monget P., Voz M.L., Belayew A., Martial J.A.;
RT "Binding of a 100-kDa ubiquitous factor to the human prolactin
RT promoter is required for its basal and hormone-regulated activity.";
RL Eur. J. Biochem. 210:53-58(1992).
DR EMBL; X00368; CAA25108.1; -; Genomic_DNA.
KW Signal.
FT SIGNAL <1 8 Potential.
FT NON TER 1 1
SQ SEQUENCE 9 AA; 1060 MW; 0A1A6775B8733054 CRC64;

Query Match 37.3%; Score 19; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GSPY 9
|:|:|
Db 5 GSPW 8

RESULT 7
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AC Q67B09;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE M4 protein (Fragment).
OS Bacteriophage b1170.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=63118;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sousa A., Ze-Ze L., Parreira R., Tenreiro R., Silva P.;
RT "Experimental phylogenies: picking a (the right) model.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

RT organization in two genes.";
RL J. Biol. Chem. 268:13010-13010(1993).
DR EMBL; S62577; AAR27101.1; -; Genomic_DNA.
FT NON TER 9
SQ SEQUENCE 9 AA; 995 MW; 8C8EA5B877376DDA CRC64;

Query Match 37.3%; Score 19; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2.2e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGVGSPY 9
|:|:|
Db 3 APLGSSY 9

RESULT 6
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AC Q9UQW0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Prolactin precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84182507; PubMed=6325171;
RA Truong A.T., Duez C., Belayew A., Renard A., Pictet R.L., Bell G.I.,
RA Martial J.A.;
RT "Isolation and characterization of the human prolactin gene.";
RL EMBO J. 3:429-437(1984).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93076813; PubMed=1332868;
RA Peers B., Naida A.M., Monget P., Voz M.L., Belayew A., Martial J.A.;
RT "Binding of a 100-kDa ubiquitous factor to the human prolactin
RT promoter is required for its basal and hormone-regulated activity.";
RL Eur. J. Biochem. 210:53-58(1992).
DR EMBL; X00368; CAA25108.1; -; Genomic_DNA.
KW Signal.
FT SIGNAL <1 8 Potential.
FT NON TER 1 1
SQ SEQUENCE 9 AA; 1060 MW; 0A1A6775B8733054 CRC64;

Query Match 37.3%; Score 19; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GSPY 9
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Db 5 GSPW 8

RESULT 7
Q67B09_9CAUD PRELIMINARY; PRT; 10 AA.
AC Q67B09;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE M4 protein (Fragment).
OS Bacteriophage b1170.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=63118;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sousa A., Ze-Ze L., Parreira R., Tenreiro R., Silva P.;
RT "Experimental phylogenies: picking a (the right) model.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY375289; AAR26461.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 10 AA; 997 MW; D38BCC44732C87D CRC64;

Query Match 37.3%; Score 19; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.7e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGV 5
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Db 1 VVAGV 5

RESULT 8
Q76MK9_9TELE PRELIMINARY; PRT; 10 AA.
AC Q76MK9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE NADH dehydrogenase subunit 2 (fragment).
GN Name=ND2;
OS Eurypharynx pelecanoides (pelican eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC Eurypharyngidae; Eurypharynx.
OX NCBI_TaxID=55117;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22967687; PubMed=12949142; DOI=10.1093/molbev/msg206;
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-
RT scale gene rearrangements originated within the eels.";
RL Mol. Biol. Evol. 20:1917-1924(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046485; BAB87156.1; -; Genomic_DNA.
DR EMBL; AB046489; BAB87164.1; -; Genomic_DNA.
DR EMBL; AB046481; BAB87148.1; -; Genomic_DNA.
GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1293 MW; 356FAE29C682DB47 CRC64;

Query Match 37.3%; Score 19; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.7e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SPYV 10
|:|:|
Db 2 NPYV 5

RESULT 9
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AC Q76MM5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE NADH dehydrogenase subunit 2 (fragment).
GN Name=ND2;
OS Eurypharynx pelecanoides (pelican eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC Eurypharyngidae; Eurypharynx.
OX NCBI_TaxID=55117;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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AC Q7SA62;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU08327.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zeiter A., Schulte U.,
RA Rothe G.O., Jedd G., Meves W., Staben C., Marcotte E., Greenberg D.,
RA Koy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cognoni C., Macino G., Catchside D., Li W., Pratt R.J., Omani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Manhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,
RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -! CAUTION: the sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000206; EAA33304.1; -; Genomic DNA.
SQ SEQUENCE 10 AA; 1284 MW; D6D34CB72DC40059 CRC64;

Query Match 35.3%; Score 18; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SPY 9
DB 8 SPY 10

RESULT 14
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ID Q60HP3 GLABR PRELIMINARY; PRT; 10 AA.
AC Q60HP3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN Name=NDL;
OS Xyrichtys dea.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidae;
OC Labridae; Xyrichtys.
OX NCBI_TaxID=242818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mabuchi K., Miya M., Satoh T.P., Westneat M.W., Nishida M.;
RT "Gene Rearrangements and Evolution of tRNA Pseudogenes in the
RT Mitochondrial Genome of the Parrotfishes (Teleostei: Perciformes:
RT Scaridae).";
RL J. Mol. Evol. 59:287-297(2004).
DR EMBL; AB117556; BAD51879.1; -; Genomic DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.

FT NON TER 1 1
SQ SEQUENCE 10 AA; 1030 MW; 4703C37760587DD7 CRC64;

Query Match 35.3%; Score 18; DB 2; Length 10;
Best Local Similarity 37.5%; Pred. No. 2.7e+04;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 MAGVGSPPY 9
DB 3 LAGIPPOY 10

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ID CIP1_MYTD STANDARD; PRT; 6 AA.
AC P13736;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Contraction-inhibiting peptide I (MIP I).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
OC Mytiloidae; Mytilidae; Mytilinae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Pedal ganglion;
RX MEDLINE=88240357; PubMed=3377776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RA "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -! FUNCTION: Inhibitory action on contractions in several molluscan
CC muscles.
CC -! SIMILARITY: To M.edulis MIP II.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A27696; A27696.
KW Amidation; Direct protein sequencing; Hormone.
PT MOD_RES 6 6
SQ SEQUENCE 6 AA; 637 MW; 72C9C66775B81000 CRC64;

Query Match 33.3%; Score 17; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GSP 3

Search completed: April 11, 2006, 19:22:35
Job time : 231 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2006, 19:34:56 ; Search time 47 Seconds  
(without alignments)  
17.591 Million cell updates/sec

Title: US-09-277-064-12

Perfect score: 51  
Sequence: 1 VNAVGVSPV 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	1	US-08-467-083-29
2	51	100.0	10	1	US-08-414-417B-29
3	51	100.0	10	1	US-08-486-348A-29
4	51	100.0	10	1	US-08-468-545B-29
5	51	100.0	10	2	US-08-466-680B-29
6	51	100.0	10	2	US-09-341-982-95
7	51	100.0	10	2	US-09-543-608A-16
8	51	100.0	10	2	US-09-354-533-29
9	51	100.0	10	4	PCT-US95-16415-12
10	51	100.0	82	2	US-09-979-338A-27
11	51	100.0	92	2	US-09-979-338A-31
12	51	100.0	265	1	US-07-857-224B-66
13	51	100.0	580	1	US-08-414-417B-69
14	51	100.0	580	1	US-08-486-348A-69
15	51	100.0	580	1	US-08-468-545B-69
16	51	100.0	580	2	US-08-466-680B-69
17	51	100.0	580	2	US-09-354-533-69
18	51	100.0	1255	1	US-08-467-083-68
19	51	100.0	1255	1	US-08-414-417B-68
20	51	100.0	1255	1	US-08-484-438-8
21	51	100.0	1255	1	US-08-486-348A-68
22	51	100.0	1255	1	US-08-625-101-2
23	51	100.0	1255	1	US-08-468-545B-68
24	51	100.0	1255	1	US-08-356-786-2
25	51	100.0	1255	2	US-08-466-680B-68
26	51	100.0	1255	2	US-09-527-487-2
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28	51	100.0	1255	2	US-09-354-533-68	Sequence 68, Appl
29	51	100.0	1255	2	US-09-441-411-6	Sequence 6, Appl
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31	47	92.2	9	2	US-09-527-487-9	Sequence 9, Appl
32	47	92.2	10	2	US-08-159-339A-263	Sequence 263, Appl
33	38	74.5	15	1	US-08-467-083-44	Sequence 44, Appl
34	38	74.5	15	1	US-08-414-417B-44	Sequence 44, Appl
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36	38	74.5	15	1	US-08-466-680B-44	Sequence 44, Appl
37	38	74.5	15	2	US-09-354-533-44	Sequence 44, Appl
38	37	72.5	132	2	US-09-328-352-5435	Sequence 5435, Ap
39	37	72.5	210	2	US-09-107-433-4914	Sequence 4914, Ap
40	37	72.5	245	2	US-09-030-978A-2	Sequence 2, Appl
41	37	72.5	245	2	US-09-583-110-5152	Sequence 5152, Ap
42	36	70.6	44	2	US-10-318-675-81	Sequence 81, Appl
43	36	70.6	44	2	US-10-318-675-83	Sequence 83, Appl
44	36	70.6	643	2	US-09-949-016-10903	Sequence 10903, A
45	36	70.6				

ALIGNMENTS

RESULT 1  
US-08-467-083-29  
; Sequence 29, Application US/08467083  
; Patent No. 5726023  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Disig, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/467,083  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/414,417  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; TELEX: 3723836 SEEDANBERRY  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-467-083-29

Query Match 100.0%; Score 51; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0097;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 VMAGVGSPPV 10

RESULT 2
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; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-414-417B-29
Query Match 100.0%; Score 51; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10
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Db 1 VMAGVGSPPV 10

RESULT 3
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; Sequence 29, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
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QY 1 VMAGVGSPPV 10
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Db 1 VMAGVGSPPV 10

RESULT 4
US-08-468-545B-29
; Sequence 29, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,545B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-486-348A-29
Query Match 100.0%; Score 51; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10
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Db 1 VMAGVGSPPV 10
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TOPOLOGY: linear  
US-08-468-545B-29

Query Match 100.0%; Score 51; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0097;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPPV 10  
Db 1 VMAGVGSPPV 10

RESULT 5  
US-08-466-680B-29  
; Sequence 29, Application US/08466680B  
; Patent No. 6075122  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Disig, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,680B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharkey, Richard G.  
; REGISTRATION NUMBER: 32,629  
; REFERENCE/DOCKET NUMBER: 920010.448C4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-466-680B-29

Query Match 100.0%; Score 51; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0097;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPPV 10  
Db 1 VMAGVGSPPV 10

RESULT 6  
US-09-341-982-95  
; Sequence 95, Application US/09341982  
; Patent No. 6558671  
; GENERAL INFORMATION:  
; APPLICANT: SLINGLUFF, Craig L.  
; APPLICANT: HUNT, Donald F.  
; APPLICANT: ENGELHARD, Victor H.  
; APPLICANT: KITTLESEN, David  
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED

TOPOLOGY: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR  
FILE REFERENCE: SLINGLUFF-3B  
CURRENT APPLICATION NUMBER: US/09/341,982  
CURRENT FILING DATE: 1999-09-20  
EARLIER APPLICATION NUMBER: PCT/US98/01592  
EARLIER FILING DATE: 1998-01-29  
EARLIER APPLICATION NUMBER: 60/037,781  
EARLIER FILING DATE: 1997-01-31  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 95  
LENGTH: 10  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Fragment of  
OTHER INFORMATION: human protein  
US-09-341-982-95

Query Match 100.0%; Score 51; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0097;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPPV 10  
Db 1 VMAGVGSPPV 10

RESULT 7  
US-09-543-608A-16  
; Sequence 16, Application US/09543608A  
; Patent No. 6602510  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John D.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa A.  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen  
; TITLE OF INVENTION: Peptides and Vaccine Compositions  
; FILE REFERENCE: 018623-015710US  
; CURRENT APPLICATION NUMBER: US/09/543,608A  
; CURRENT FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 10  
; TYPE: PPT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Her2/neu.773  
US-09-543-608A-16

Query Match 100.0%; Score 51; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0097;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPPV 10  
Db 1 VMAGVGSPPV 10

RESULT 8  
US-09-354-533-29  
; Sequence 29, Application US/09354533  
; Patent No. 6664370  
; GENERAL INFORMATION:  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: Disig, Mary L.  
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
HER-2/neu ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/354,533

FILING DATE: 15-Jul-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C9

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 29:

US-09-354-533-29

Query Match 100.0%; Score 51; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0097;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10

Db 1 VMAGVGSPPV 10

RESULT 9  
PCT-US95-16415-12  
Sequence 12, Application PC/TUS9516415  
GENERAL INFORMATION:  
APPLICANT: The Scripps Research Institute  
TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC  
TITLE OF INVENTION: CYTOTOXIC T CELLS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute  
STREET: 10666 North Torrey Pines Road, TPC-8  
CITY: La Jolla  
STATE: California  
COUNTRY: US  
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/16415

FILING DATE: 13-DEC-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/355,558

FILING DATE: 14-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Logan, April C.

REGISTRATION NUMBER: 33,950  
REFERENCE/DOCKET NUMBER: 433.1PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 554-2937  
TELEFAX: (619) 554-6312  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
PCT-US95-16415-12

Query Match 100.0%; Score 51; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0097;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10

Db 1 VMAGVGSPPV 10

RESULT 10  
US-09-979-338A-27  
Sequence 27, Application US/09979338A  
Patent No. 6846622  
GENERAL INFORMATION:  
APPLICANT: Heffron et al.  
TITLE OF INVENTION: Tagged Epitope Protein Transposable Element  
FILE REFERENCE: 61589  
CURRENT APPLICATION NUMBER: US/09/979,338A  
CURRENT FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: PCT/US00/14687  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/136,210  
PRIOR FILING DATE: 1999-05-26  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 27  
LENGTH: 82  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
OTHER INFORMATION: resolved product using the construct shown in FIG  
OTHER INFORMATION: 5.  
US-09-979-338A-27

Query Match 100.0%; Score 51; DB 2; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.077;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10

Db 40 VMAGVGSPPV 49

RESULT 11  
US-09-979-338A-31  
Sequence 31, Application US/09979338A  
Patent No. 6846622  
GENERAL INFORMATION:  
APPLICANT: Heffron et al.  
TITLE OF INVENTION: Tagged Epitope Protein Transposable Element  
FILE REFERENCE: 61589  
CURRENT APPLICATION NUMBER: US/09/979,338A  
CURRENT FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: PCT/US00/14687  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/136,210  
PRIOR FILING DATE: 1999-05-26  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 31  
LENGTH: 92  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
OTHER INFORMATION: resolved product using the construct shown in f  
OTHER INFORMATION: FIG 9.  
US-09-979-338A-31

Query Match 100.0%; Score 51; DB 2; Length 92;  
Best Local Similarity 100.0%; Pred. No. 0.086; 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
DB 47 VMAGVGSPPV 56  
|||||

RESULT 12  
US-07-857-224B-66  
Sequence 66, Application US/07857224B  
Patent No. 5958784  
GENERAL INFORMATION:  
APPLICANT: Benner, Steven A.  
TITLE OF INVENTION: Predicting Folded Structures of Proteins  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Steven A. Benner  
STREET: Hadlaubstrasse 151  
CITY: Zurich  
STATE: none  
COUNTRY: Switzerland  
ZIP: (note: this is an international post code) CH-8092

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.4 MB storage  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
FILING DATE: 03/25/92  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA: none  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (International) 41 1 632 2830  
TELEFAX: (International) 41 1 262 2437  
TELEX: none  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 265  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: protein  
ORIGINAL SOURCE:  
ORGANISM: human  
FEATURE: Protein kinase; Table 8 Column 75  
PUBLICATION INFORMATION:  
AUTHORS:  
AUTHORS: Hanks, S. K.  
AUTHORS: Quinn, A. M.  
AUTHORS: Hunter, T.  
TITLE: The protein kinase family  
JOURNAL: Science  
VOLUME: 241  
PAGES: 42-52  
DATE: 1988

Query Match 100.0%; Score 51; DB 1; Length 265;  
Best Local Similarity 100.0%; Pred. No. 0.24; 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
DB 56 VMAGVGSPPV 65  
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RESULT 13  
US-08-414-417B-69  
Sequence 69, Application US/08414417B  
Patent No. 5801005  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/414,417B  
FILING DATE: 31-MAR-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharkey, Richard G.  
REGISTRATION NUMBER: 32,629  
REFERENCE/DOCKET NUMBER: 920010.448C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 580 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-414-417B-69

Query Match 100.0%; Score 51; DB 1; Length 580;  
Best Local Similarity 100.0%; Pred. No. 0.52; 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
DB 98 VMAGVGSPPV 107  
|||||

RESULT 14  
US-08-486-348A-69  
Sequence 69, Application US/08486348A  
Patent No. 5846538  
GENERAL INFORMATION:  
APPLICANT: Cheever, Martin A.  
APPLICANT: Disis, Mary L.  
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington

```
;
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-486-348A-69.

Query Match 100.0%; Score 51; DB 1; Length 580;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPYV 10
DB 98 VMAGVGSPYV 107

Search completed: April 11, 2006, 19:36:15
Job time : 47 secs

;
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-468-545B-69

Query Match 100.0%; Score 51; DB 1; Length 580;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPYV 10
DB 98 VMAGVGSPYV 107

Search completed: April 11, 2006, 19:36:15
Job time : 47 secs

;
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,545B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-468-545B-69.

Query Match 100.0%; Score 51; DB 1; Length 580;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPYV 10
DB 98 VMAGVGSPYV 107

RESULT 15
US-08-468-545B-69
; Sequence 69, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,545B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 amino acids
; TYPE: amino acid
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2006, 19:35:40 ; Search time 166 Seconds  
(without alignments)  
25.170 Million cell updates/sec

Title: US-09-277-064-12

Perfect score: 51

Sequence: 1 VMAGVGSPPV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pcp.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pcp.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pcp.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pcp.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pcp.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	2	US-08-812-393A-49
2	51	100.0	10	3	US-09-354-533-29
3	51	100.0	10	3	US-09-277-074-12
4	51	100.0	10	3	US-09-277-064-12
5	51	100.0	10	3	US-09-774-681-49
6	51	100.0	10	4	US-10-080-013-16
7	51	100.0	10	4	US-10-245-871-620
8	51	100.0	10	4	US-10-149-138-786
9	51	100.0	10	4	US-10-149-138-2352
10	51	100.0	10	4	US-10-149-138-4335
11	51	100.0	10	4	US-10-149-138-4422
12	51	100.0	10	4	US-10-149-138-4435
13	51	100.0	10	4	US-10-253-286-620
14	51	100.0	10	4	US-10-289-566-16
15	51	100.0	10	4	US-10-333-430-31
16	51	100.0	10	4	US-10-647-005-29
17	51	100.0	10	4	US-10-149-138-786
18	51	100.0	10	4	US-10-149-138-2352
19	51	100.0	10	4	US-10-149-138-4335
20	51	100.0	10	4	US-10-149-138-4422
21	51	100.0	10	4	US-10-149-138-4435
22	51	100.0	10	6	US-11-121-347-29
23	51	100.0	11	4	US-10-149-138-838
24	51	100.0	11	4	US-10-149-138-2386
25	51	100.0	11	4	US-10-149-138-838
26	51	100.0	11	4	US-10-149-138-2386
27	51	100.0	15	4	US-10-149-138-3728

28	51	100.0	15	4	US-10-149-138-3736	Sequence 3736, Ap
29	51	100.0	15	4	US-10-149-138-4473	Sequence 4473, Ap
30	51	100.0	15	4	US-10-149-138-4500	Sequence 4500, Ap
31	51	100.0	15	4	US-10-149-138-4562	Sequence 4562, Ap
32	51	100.0	15	4	US-10-149-138-3728	Sequence 3728, Ap
33	51	100.0	15	4	US-10-149-138-3736	Sequence 3736, Ap
34	51	100.0	15	4	US-10-149-138-4473	Sequence 4473, Ap
35	51	100.0	15	4	US-10-149-138-4500	Sequence 4500, Ap
36	51	100.0	15	4	US-10-149-138-4562	Sequence 4562, Ap
37	51	100.0	18	3	US-09-734-520-24	Sequence 24, Appl
38	51	100.0	18	4	US-10-012-034A-24	Sequence 24, Appl
39	51	100.0	23	4	US-10-245-871-622	Sequence 622, App
40	51	100.0	23	4	US-10-253-286-622	Sequence 622, App
41	51	100.0	126	4	US-10-333-430-70	Sequence 70, Appl
42	51	100.0	171	5	US-10-482-029-247	Sequence 247, Appl
43	51	100.0	289	5	US-10-801-266-6	Sequence 6, Appl
44	51	100.0	391	5	US-10-949-667-6	Sequence 6, Appl
45	51	100.0	570	4	US-10-378-393-15	Sequence 15, Appl

#### ALIGNMENTS

##### RESULT 1

US-08-812-393A-49

; Sequence 49, Application US/08812393A

; Publication No. US20010007152A1

; GENERAL INFORMATION:

; APPLICANT: SHERMAN, Linda A.

; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING

; TITLE OF INVENTION: T CELL RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR

; TITLE OF INVENTION: ANTIGENS

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 2000 Pennsylvania Avenue, NW, suite 5500

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20006-1888

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/812.393A

; FILING DATE: 05-MAR-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Murashige, Kate H

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 31333-20001.00

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-887-1500

; TELEFAX: 202-822-0168

; TELEX:

; INFORMATION FOR SEQ ID NO: 49:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-812-393A-49

Query Match 100.0%; Score 51; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VMAGVGSPPV 10
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Db      1 VMAGVGSPPV 10

RESULT 2
US-09-354-533-29
; Sequence 29, Application US/09354533
; Publication No. US20020055614A1
; GENERAL INFORMATION:
; APPLICANT: Creever, Martin A.
; DISCLOSURE: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/354,533
; APPLICATION NUMBER: US/09/354,533
; FILING DATE: 15-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-354-533-29

Query Match      100.0%; Score 51; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VMAGVGSPPV 10
      |||||
Db      1 VMAGVGSPPV 10

RESULT 3
US-09-277-074-12
; Sequence 12, Application US/09277074
; Publication No. US20030022820A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Linda A.
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
; FILE REFERENCE: SCR2155S
; CURRENT APPLICATION NUMBER: US/09/277,074
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/355,558
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: PCT/US95/16415
; PRIOR FILING DATE: 1995-12-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.1
US-09-277-074-12

Query Match      100.0%; Score 51; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VMAGVGSPPV 10
      |||||
Db      1 VMAGVGSPPV 10

RESULT 4
US-09-277-064-12
; Sequence 12, Application US/09277064
; Publication No. US20030064916A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Linda A.
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
; FILE REFERENCE: SCR2152S
; CURRENT APPLICATION NUMBER: US/09/277,064
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/355,558
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: PCT/US95/16415
; PRIOR FILING DATE: 1995-12-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.1
US-09-277-064-12

Query Match      100.0%; Score 51; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VMAGVGSPPV 10
      |||||
Db      1 VMAGVGSPPV 10

RESULT 5
US-09-774-681-49
; Sequence 49, Application US/09774681
; Publication No. US20030208780A1
; GENERAL INFORMATION:
; APPLICANT: Sunol Molecular Corporation
; APPLICANT: Sherman, Linda
; APPLICANT: Lustgarten, Joseph
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING T CELL
; TITLE OF INVENTION: RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS
; FILE REFERENCE: 31333-20001.01
; CURRENT APPLICATION NUMBER: US/09/774,681
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: US 08/812,393
; PRIOR FILING DATE: 1997-03-05
; PRIOR APPLICATION NUMBER: US 60/012,845
; PRIOR FILING DATE: 1996-03-05
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
US-09-774-681-49

Query Match      100.0%; Score 51; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VMAGVGSPPV 10
      |||||
Db      1 VMAGVGSPPV 10

RESULT 6
US-09-774-681-49
; Sequence 49, Application US/09774681
; Publication No. US20030208780A1
; GENERAL INFORMATION:
; APPLICANT: Sunol Molecular Corporation
; APPLICANT: Sherman, Linda
; APPLICANT: Lustgarten, Joseph
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING T CELL
; TITLE OF INVENTION: RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS
; FILE REFERENCE: 31333-20001.01
; CURRENT APPLICATION NUMBER: US/09/774,681
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: US 08/812,393
; PRIOR FILING DATE: 1997-03-05
; PRIOR APPLICATION NUMBER: US 60/012,845
; PRIOR FILING DATE: 1996-03-05
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
US-09-774-681-49

Query Match      100.0%; Score 51; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VMAGVGSPPV 10
      |||||
Db      1 VMAGVGSPPV 10

RESULT 7
US-09-277-074-12
; Sequence 12, Application US/09277074
; Publication No. US20030022820A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Linda A.
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
; FILE REFERENCE: SCR2155S
; CURRENT APPLICATION NUMBER: US/09/277,074
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/355,558
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: PCT/US95/16415
; PRIOR FILING DATE: 1995-12-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.1
US-09-277-074-12
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Query Match 100.0%; Score 51; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
Db 1 VMAGVGSPPV 10

## RESULT 6

US-10-080-013-16  
; Sequence 16, Application US/10080013  
; Publication No. US2003007248A1  
; GENERAL INFORMATION:  
; APPLICANT: Moriarty, Ann  
; APPLICANT: Leturcq, Didier  
; APPLICANT: Degraw, Juli  
; APPLICANT: Heiskala, Marja  
; APPLICANT: Peterson, Per  
; APPLICANT: Jackson, Michael  
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS  
; FILE REFERENCE: ORT-1557  
; CURRENT APPLICATION NUMBER: US/10/080,013  
; CURRENT FILING DATE: 2002-02-19  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-080-013-16

Query Match 100.0%; Score 51; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
Db 1 VMAGVGSPPV 10

## RESULT 7

US-10-245-871-620  
; Sequence 620, Application US/10245871  
; Publication No. US2003023594A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2013  
; CURRENT APPLICATION NUMBER: US/10/245,871  
; CURRENT FILING DATE: 2003-01-09  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1993-09-14  
; NUMBER OF SEQ ID NOS: 905  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 620  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-245-871-620

Query Match 100.0%; Score 51; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
Db 1 VMAGVGSPPV 10

## RESULT 8

US-10-149-138-786  
; Sequence 786, Application US/10149138  
; Publication No. US20040018971A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
; FILE REFERENCE: 2060.0140001  
; CURRENT APPLICATION NUMBER: US/10/149,138  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: PCT/US00/33591  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/458,299  
; PRIOR FILING DATE: 1999-12-11  
; NUMBER OF SEQ ID NOS: 4641  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 786  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-786

Query Match 100.0%; Score 51; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
Db 1 VMAGVGSPPV 10

## RESULT 9

US-10-149-138-2352  
; Sequence 2352, Application US/10149138  
; Publication No. US20040018971A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions  
; FILE REFERENCE: 2060.0140001  
; CURRENT APPLICATION NUMBER: US/10/149,138  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: PCT/US00/33591  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/458,299  
; PRIOR FILING DATE: 1999-12-11  
; NUMBER OF SEQ ID NOS: 4641  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2352  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-2352

Query Match 100.0%; Score 51; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.016;

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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10
   |||||
Db 1 VMAGVGSPPV 10

RESULT 10
US-10-149-138-4335
; Sequence 4335, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4335
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4335

Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10
   |||||
Db 1 VMAGVGSPPV 10

RESULT 11
US-10-149-138-4422
; Sequence 4422, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4422
; LENGTH: 10
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4422

Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10
   |||||
Db 1 VMAGVGSPPV 10

RESULT 12
US-10-149-138-4435
; Sequence 4435, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4435
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4435

Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10
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Db 1 VMAGVGSPPV 10

RESULT 13
US-10-253-286-620
; Sequence 620, Application US/10253286
; Publication No. US20040058891A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; CURRENT APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 620
; LENGTH: 10
; TYPE: PRT
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-286-620

Query Match      100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VMAGVGSPPV 10
      |||||
Db      1 VMAGVGSPPV 10

RESULT 14
US-10-289-566-16
; Sequence 16, Application US/10289566
; Publication No. US20040071671A1
; GENERAL INFORMATION:
; APPLICANT: Leturcq, Didier J.
; APPLICANT: Moriarty, Ann M.
; APPLICANT: Jackson, Michael R.
; APPLICANT: Peterson, Per A.
; APPLICANT: Richards, Jon M.
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT 1342CIP
; CURRENT APPLICATION NUMBER: US/10/289,566
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/270,252
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: US 10/080,013
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-289-566-16

Query Match      100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VMAGVGSPPV 10
      |||||
Db      1 VMAGVGSPPV 10

RESULT 15
US-10-333-430-31
; Sequence 31, Application US/10333430
; Publication No. US20040072240A1
; GENERAL INFORMATION:
; APPLICANT: INSERM
; APPLICANT: INSTITUT GUSTAVE ROUSSY
; APPLICANT: KOSMATOPOULOS, Kostas
; APPLICANT: TOURDOT, Sophie
; APPLICANT: SCARDINO, Antonio
; APPLICANT: GROSS, David, Alexandre
; TITLE OF INVENTION: METHOD FOR SCREENING PEPTIDES FOR USE IN
; TITLE OF INVENTION: IMMUNOTHERAPY
; FILE REFERENCE: 33339/259034
; CURRENT APPLICATION NUMBER: US/10/333,430
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: FR 0009591
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-333-430-31

Query Match      100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VMAGVGSPPV 10
      |||||
Db      1 VMAGVGSPPV 10

Search completed: April 11, 2006, 19:39:07
Job time : 167 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2006, 19:36:30 ; Search time 25 Seconds  
(without alignments)  
12.477 Million cell updates/sec

Title: US-09-277-064-12

Perfect score: 51

Sequence: 1 VMAGVGSPV 10

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New.\*

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2: /SID55/ptodata/1/pubpaa/US06 NEW PUB pep.\*  
3: /SID55/ptodata/1/pubpaa/US07 NEW PUB pep.\*  
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5: /SID55/ptodata/1/pubpaa/US09 NEW PUB pep.\*  
6: /SID55/ptodata/1/pubpaa/US10 NEW PUB pep.\*  
7: /SID55/ptodata/1/pubpaa/US11 NEW PUB pep.\*  
8: /SID55/ptodata/1/pubpaa/US60 NEW PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	51	100.0	10	7	US-11-033-039-620
2	51	100.0	23	7	US-11-033-039-622
3	51	100.0	82	6	US-10-968-629-27
4	51	100.0	92	6	US-10-968-629-31
5	51	100.0	1255	6	US-10-770-726-62
6	51	100.0	1255	7	US-11-022-562-213
7	51	100.0	1255	7	US-11-113-202-10
8	51	100.0	1255	7	US-11-033-039-553
9	51	100.0	1255	7	US-11-155-288-9
10	51	100.0	1255	7	US-11-202-516-4
11	51	100.0	1255	7	US-11-175-405-2
12	51	100.0	1258	7	US-11-033-039-930
13	42	82.4	19	7	US-11-033-039-931
14	41	80.4	9	6	US-10-910-101-135
15	38	74.5	15	7	US-11-033-039-908
16	38	74.5	20	7	US-11-033-039-932
17	36	70.6	44	6	US-10-957-887B-209
18	36	70.6	44	6	US-10-957-887B-251
19	36	70.6	161	7	US-11-098-686-11415
20	35	68.6	19	7	US-11-033-039-933
21	35	68.6	217	7	US-11-096-568A-16847
22	35	68.6	506	7	US-11-055-822-946
23	35	68.6	730	7	US-11-082-389-358
24	34	66.7	374	7	US-11-072-175-148
25	34	66.7	435	7	US-11-087-099-3138

26 34 66.7 462 7 US-11-082-389-412 Sequence 412, App  
27 34 66.7 1433 7 US-11-094-519A-40 Sequence 40, Appl  
28 33 64.7 112 7 US-11-230-180-17 Sequence 17, Appl  
29 33 64.7 358 7 US-11-087-099-11741 Sequence 11741, A  
30 33 64.7 363 7 US-11-087-099-2715 Sequence 2715, Ap  
31 33 64.7 363 7 US-11-087-099-3776 Sequence 3776, Ap  
32 33 64.7 363 7 US-11-087-099-4337 Sequence 4337, Ap  
33 33 64.7 491 7 US-11-098-686-10836 Sequence 10836, A  
34 33 64.7 748 7 US-11-096-568A-34369 Sequence 34369, A  
35 32 62.7 208 7 US-11-096-568A-22891 Sequence 22891, A  
36 32 62.7 237 7 US-11-096-568A-33599 Sequence 33599, A  
37 32 62.7 256 7 US-11-096-568A-32890 Sequence 32890, A  
38 32 62.7 284 7 US-11-096-568A-33598 Sequence 33598, A  
39 32 62.7 313 7 US-11-087-099-257 Sequence 257, App  
40 32 62.7 313 7 US-11-096-568A-33597 Sequence 33597, A  
41 32 62.7 324 7 US-11-087-099-10913 Sequence 10913, A  
42 32 62.7 324 7 US-11-051-720-1349 Sequence 1349, Ap  
43 32 62.7 344 7 US-11-087-099-7157 Sequence 7157, Ap  
44 32 62.7 362 7 US-11-087-099-1068 Sequence 1068, Ap  
45 32 62.7 369 7 US-11-087-099-9241 Sequence 9241, Ap

#### ALIGNMENTS

RESULT 1  
US-11-033-039-620  
; Sequence 620, Application US/11033039  
; Publication No. US20060002947A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2017US01  
; CURRENT APPLICATION NUMBER: US/11/033,039  
; CURRENT FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: 10/245,871  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 1452  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 620  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-033-039-620

Query Match 100.0%; Score 51; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.00065;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSPV 10  
Db 1 VMAGVGSPV 10

RESULT 2  
US-11-033-039-622  
; Sequence 622, Application US/11033039  
; Publication No. US20060002947A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2017US01  
; CURRENT APPLICATION NUMBER: US/11/033,039  
; CURRENT FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: 10/245,871  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: 10/197,000

;/ CURRENT FILING DATE: 2002-07-17  
;/ PRIOR APPLICATION NUMBER: 09/396,813  
;/ PRIOR FILING DATE: 1999-09-14  
;/ NUMBER OF SEQ ID NOS: 1452  
;/ SOFTWARE: PatentIn version 3.3  
;/ SEQ ID NO 622  
;/ LENGTH: 23  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;/ OTHER INFORMATION: hybrid peptide  
;/ NAME/KEY: MOD.RES  
;/ LOCATION: (5)..(5)  
;/ OTHER INFORMATION: Avá  
US-11-033-039-622

Query Match 100.0%; Score 51; DB 7; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.0016;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
Db 6 VMAGVGSPPV 15  
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RESULT 3  
US-10-968-629-27  
;/ Sequence 27, Application US/10968629  
;/ Publication No. US20060040382A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Heifron et al.  
;/ TITLE OF INVENTION: Tagged Epitope Protein Transposable Element  
;/ FILE REFERENCE: 61589  
;/ CURRENT FILING DATE: 2004-10-18  
;/ PRIOR APPLICATION NUMBER: US/10/968,629  
;/ PRIOR FILING DATE: 2001-11-21  
;/ PRIOR APPLICATION NUMBER: PCT/US00/14687  
;/ PRIOR FILING DATE: 2000-05-26  
;/ PRIOR APPLICATION NUMBER: 60/136,210  
;/ PRIOR FILING DATE: 1999-05-26  
;/ NUMBER OF SEQ ID NOS: 33  
;/ SOFTWARE: PatentIn ver. 2.1  
;/ SEQ ID NO 27  
;/ LENGTH: 82  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
;/ OTHER INFORMATION: resolved product using the construct shown in FIG  
;/ OTHER INFORMATION: 5.  
US-10-968-629-27

Query Match 100.0%; Score 51; DB 6; Length 82;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
Db 40 VMAGVGSPPV 49  
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RESULT 4  
US-10-968-629-31  
;/ Sequence 31, Application US/10968629  
;/ Publication No. US20060040382A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Heifron et al.  
;/ TITLE OF INVENTION: Tagged Epitope Protein Transposable Element  
;/ FILE REFERENCE: 61589  
;/ CURRENT APPLICATION NUMBER: US/10/968,629

;/ CURRENT FILING DATE: 2004-10-18  
;/ PRIOR APPLICATION NUMBER: 09/979,338  
;/ PRIOR FILING DATE: 2001-11-21  
;/ PRIOR APPLICATION NUMBER: PCT/US00/14687  
;/ PRIOR FILING DATE: 2000-05-26  
;/ PRIOR APPLICATION NUMBER: 60/136,210  
;/ PRIOR FILING DATE: 1999-05-26  
;/ NUMBER OF SEQ ID NOS: 33  
;/ SOFTWARE: PatentIn ver. 2.1  
;/ SEQ ID NO 31  
;/ LENGTH: 92  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
;/ OTHER INFORMATION: resolved product using the construct shown in f  
;/ OTHER INFORMATION: FIG 9.  
US-10-968-629-31

Query Match 100.0%; Score 51; DB 6; Length 92;  
Best Local Similarity 100.0%; Pred. No. 0.0072;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
Db 47 VMAGVGSPPV 56  
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RESULT 5  
US-10-770-726-62  
;/ Sequence 62, Application US/10770726  
;/ Publication No. US20050266409A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Wyeth  
;/ APPLICANT: Liu, Wei  
;/ APPLICANT: Brown, Eugene  
;/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATI  
;/ TITLE OF INVENTION: CANCERS  
;/ FILE REFERENCE: AM101079 (031896-010000)  
;/ CURRENT APPLICATION NUMBER: US/10/770,726  
;/ CURRENT FILING DATE: 2004-02-04  
;/ NUMBER OF SEQ ID NOS: 48640  
;/ SOFTWARE: PatentIn version 3.2  
;/ SEQ ID NO 62  
;/ LENGTH: 1255  
;/ TYPE: PRT  
;/ ORGANISM: Homo sapiens  
US-10-770-726-62

Query Match 100.0%; Score 51; DB 6; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
Db 773 VMAGVGSPPV 782  
|||||

RESULT 6  
US-11-022-562-213  
;/ Sequence 213, Application US/11022562  
;/ Publication No. US20050249742A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Ruprecht, Ruth M.  
;/ APPLICANT: Shisong, Jiang  
;/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING  
;/ TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE  
;/ FILE REFERENCE: DFN-043CN  
;/ CURRENT APPLICATION NUMBER: US/11/022,562  
;/ CURRENT FILING DATE: 2004-12-22  
;/ PRIOR APPLICATION NUMBER: PCT/US03/20322  
;/ PRIOR FILING DATE: 2003-06-27  
;/ PRIOR APPLICATION NUMBER: 60/392718

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; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-022-562-213

Query Match      100.0%; Score 51; DB 7; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VMAGVGSPPV 10
Db      773 VMAGVGSPPV 782

RESULT 7
US-11-113-202-10
; Sequence 10, Application US/11113202
; Publication No. US20050272637A1
; GENERAL INFORMATION:
; APPLICANT: Clinton, Gail M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING SIGNALING BY IGF-1
; FILE REFERENCE: 49321-136
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/590,473
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 60/564,893
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-202-10

Query Match      100.0%; Score 51; DB 7; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VMAGVGSPPV 10
Db      773 VMAGVGSPPV 782

RESULT 8
US-11-033-039-553
; Sequence 553, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: US/11/033,039
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 553
; LENGTH: 1255
; TYPE: PRT

; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-553

Query Match      100.0%; Score 51; DB 7; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VMAGVGSPPV 10
Db      773 VMAGVGSPPV 782

RESULT 9
US-11-155-288-9
; Sequence 9, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; FILE REFERENCE: MANNK.050A
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US/11/155,288
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-9

Query Match      100.0%; Score 51; DB 7; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VMAGVGSPPV 10
Db      773 VMAGVGSPPV 782

RESULT 10
US-11-202-516-4
; Sequence 4, Application US/11202516
; Publication No. US20060008465A1
; GENERAL INFORMATION:
; APPLICANT: Mouritsen, Soren
; APPLICANT: Steinna, Lucilla
; APPLICANT: Gautam, Anand
; APPLICANT: Dalum, Iben
; APPLICANT: Haaning, Jesper
; APPLICANT: Leach, Dana
; APPLICANT: Nielsen, Klaus
; APPLICANT: Karlsson, Gunilla
; APPLICANT: Rasmussen, Peter
; TITLE OF INVENTION: Novel Methods for Therapeutic Vaccination
; FILE REFERENCE: 4614-0107PUS2
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/11/202,516
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: PCT/DK99/00525
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: DK 1998 01261
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: US 60/105,011
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1255
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; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-033-039-930

Query Match 100.0%; Score 51; DB 7; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVSPYV 10  
Db 773 VMAGVSPYV 782

## RESULT 11

US-11-033-039-930  
; Sequence 2, Application US/11033039  
; Publication No. US20060002947A1  
; GENERAL INFORMATION:  
; APPLICANT: STUART, SUSAN G.  
; APPLICANT: MONAHAN, JOHN J.  
; APPLICANT: LANGTON, BEATRICE CLAUDIA  
; APPLICANT: HANCOCK, MIRIAM E.C.  
; APPLICANT: CHAO, LORRINE A.  
; APPLICANT: BLUFORD, PETER  
; TITLE OF INVENTION: C-ERBB-2 EXTERNAL DOMAIN: GP75  
; FILE REFERENCE: BEBIO-111-C1  
; CURRENT APPLICATION NUMBER: US/11/033,039  
; CURRENT FILING DATE: 2005-07-07  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 1255  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-033-039-930

Query Match 100.0%; Score 51; DB 7; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVSPYV 10  
Db 773 VMAGVSPYV 782

## RESULT 12

US-11-033-039-930  
; Sequence 930, Application US/11033039  
; Publication No. US20060002947A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2017US01  
; CURRENT APPLICATION NUMBER: US/11/033,039  
; CURRENT FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: 10/245,871  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 1452  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 930  
; LENGTH: 1258  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-033-039-930

Query Match 100.0%; Score 51; DB 7; Length 1258;  
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVSPYV 10  
Db 773 VMAGVSPYV 782

## RESULT 13

US-11-033-039-931  
; Sequence 931, Application US/11033039  
; Publication No. US20060002947A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2017US01  
; CURRENT APPLICATION NUMBER: US/11/033,039  
; CURRENT FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: 10/245,871  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 1452  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 931  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: hybrid peptide  
US-11-033-039-931

Query Match 82.4%; Score 42; DB 7; Length 19;  
Best Local Similarity 88.9%; Pred. No. 0.068;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 VMAGVSPYV 10  
Db 3 MKGVGSPYV 11

## RESULT 14

US-10-510-101-135  
; Sequence 135, Application US/10510101  
; Publication No. US20060018915A1  
; GENERAL INFORMATION:  
; APPLICANT: Epimmune Inc.  
; APPLICANT: Ishioka, Glenn  
; APPLICANT: Fikes, John  
; APPLICANT: Tangri, Shabnam  
; APPLICANT: Sette, Alessandro  
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods  
; FILE REFERENCE: 2060, 009PC05  
; CURRENT APPLICATION NUMBER: US/10/510,101  
; CURRENT FILING DATE: 2004-10-05  
; PRIOR APPLICATION NUMBER: US 60/413,471  
; PRIOR FILING DATE: 2002-09-26  
; PRIOR APPLICATION NUMBER: US 10/116,118  
; PRIOR FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 135  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide derived from Homo sapiens Her2/neu  
US-10-510-101-135

Query Match 80.4%; Score 41; DB 6; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.4e+05;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VMAGVGSFY 9  
|||  
Db 1 VMDGVGSFY 9

## RESULT 15

US-11-033-039-908  
; Sequence 908, Application US/11033039  
; Publication No. US2006002947A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2017US01  
; CURRENT APPLICATION NUMBER: US/11/033,039  
; CURRENT FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: 10/245,871  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 1452  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 908  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-033-039-908

Query Match 74.5%; Score 38; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GVGSPYV 10  
|||||  
Db 1 GVGSPYV 7

Search completed: April 11, 2006, 19:39:38  
Job time : 26 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2006, 19:31:00 ; Search time 38 Seconds  
(without alignments)  
25.320 Million cell updates/sec

Title: US-09-277-064-12

Perfect score: 51

Sequence: 1 VMAGVGSPYV 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:\*\*

1: Piri:\*\*

2: Piri:\*\*

3: Piri:\*\*

4: Piri:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	1255	1 A24571	protein-tyrosine k
2	51	100.0	1260	1 TVRTNU	protein-tyrosine k
3	48	94.1	1254	2 I48161	p-185 precursor
4	39	76.5	348	2 T09037	hypothetical prote
5	38	74.5	381	2 A69091	cell division prot
6	38	74.5	697	1 S04987	SITS-binding prote
7	37	72.5	247	2 B95109	uridylylate kinase [
8	37	72.5	247	2 E97977	UMP kinase (EC 2.7
9	37	72.5	288	2 F07800	hypothetical prote
10	37	72.5	388	2 G90450	hypothetical prote
11	37	72.5	1020	2 D83679	hypothetical prote
12	36	70.6	66	2 T35138	hypothetical prote
13	36	70.6	224	2 D46177	enhancer of split
14	36	70.6	275	1 WMBEH4	UL34 protein - hum
15	36	70.6	625	2 S65829	hypothetical prote
16	36	70.6	639	2 B48189	sodium/phosphate c
17	36	70.6	921	2 AC1327	isoleucyl-tRNA syn
18	36	70.6	921	2 AE1998	isoleucyl-tRNA syn
19	35	68.6	261	2 E83150	hypothetical prote
20	35	68.6	277	2 AD3358	2-dehydro-3-deoxy-
21	35	68.6	286	2 S76153	hypothetical prote
22	35	68.6	288	2 AI1966	permease protein o
23	35	68.6	435	2 AD2583	two component sens
24	35	68.6	481	2 B97365	helo protein U4905
25	35	68.6	529	1 H70736	IMP dehydrogenase
26	35	68.6	529	1 S72823	IMP dehydrogenase
27	35	68.6	598	2 S10893	transforming prote
28	35	68.6	616	1 RRVOLL	probable RNA-direc
29	35	68.6	616	1 RRVQWA	probable RNA-direc

#### ALIGNMENTS

##### RESULT 1

A24571

protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human

N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein er

C;Species: Homo sapiens (man)

C;Date: 25-Oct-1987 #sequence revision 06-Dec-1996 #text change 05-Oct-2004

C;Accession: A24571; A24591; A4188; B44188; I59509; I57622

R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.

Nature 319, 230-234, 1986

A;Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth

A;Reference number: A24571; MUID:86118663; PMID:3003577

A;Accession: A24571

A;Molecule type: mRNA

A;Residues: 1-1255 <YAM>

A;Cross-references: UNIPROT:P04626; UNIPARC:UPI000003F55F; GB:X03363; NID:g31197; PIDN

R;Semba, K.; Kanata, N.; Toyoshima, K.; Yamamoto, T.

Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985

A;Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epide

A;Reference number: A25491; MUID:86016729; PMID:2995967

A;Accession: A25491

A;Molecule type: DNA

A;Residues: 737-1031 <SEM>

A;Cross-references: UNIPARC:UPI000016A8A7; GB:M11767; NID:g182163; PIDN:AAA35808.1; PI

R;Cousens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, B.; Gray, A.; McGrath, J.; Seeburg,

Science 230, 1132-1139, 1985

A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chrom

A;Reference number: A44188; MUID:86070181; PMID:2999974

A;Accession: A44188

A;Molecule type: DNA

A;Residues: 740-910 <COU1>

A;Cross-references: UNIPARC:UPI000016AA26; GB:M12036; NID:g183988; PIDN:AAA35978.1; PI

A;Accession: B44188

A;Molecule type: mRNA

A;Residues: 1-517, 'RALL', 522, 'S', 524-654, 'V', 656-1169, 'A', 1171-1255 <COU2>

A;Cross-references: UNIPARC:UPI00001725C7; GB:M11730; NID:g183986

R;King, C.R.; Kraus, M.H.; Aaronson, S.A.

Science 229, 974-976, 1985

A;Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.

A;Reference number: I59509; MUID:85272597; PMID:2992089

A;Accession: I59509

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 832-909 <REX>

A;Cross-references: UNIPARC:UPI0000070A3F; GB:L29395; NID:g459807; PIDN:AAA35809.1; PI

R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.

Mol. Cell. Biol. 7, 2997-2601, 1987

A;Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcription:

A;Reference number: I57622; MUID:87286898; PMID:3039351

A;Accession: I57622

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-191 <TAU>

A;Cross-references: UNIPARC:UPI0000000427; GB:M16792; NID:G183983; PIDN:AA58637.1; PID:  
 C;Comment: Amplification and overexpression of this erbB-related gene occurs in about 30  
 C;Genetics:  
 A;Gene: GDB:ERBB2; NGL; NEU; HER-2  
 A;Cross-references: GDB:120613; OMIM:164870  
 A;Map position: 17q21.1-17q21.1  
 A;Introns: 25/1; 75/3; 147/1; 883/3  
 A;Note: the list of introns is incomplete  
 C;Function:  
 A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP  
 A;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology  
 C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosph  
 inase  
 F;1-21/Domain: signal sequence #status predicted <SIG>  
 F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>  
 F;22-653/Domain: extracellular #status predicted <EXT>  
 F;70-304/Domain: EGF receptor extracellular domain repeat <EE1>  
 F;395-605/Domain: EGF receptor extracellular domain repeat <EE2>  
 F;654-675/Domain: transmembrane #status predicted <TM>  
 F;676-1255/Domain: intracellular #status predicted <INT>  
 F;718-983/Domain: protein kinase homology <KIN>  
 F;726-734/Region: protein kinase ATP-binding motif  
 F;68-124.187.259.530.571.629/Binding site: carbohydrate (Asn) (covalent) #status predict  
 F;686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
 F;753/Active site: Lys #status predicted  
 F;1139.1221.1222.1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)  
 Query Match 100.0%; Score 51; DB 1; Length 1255;  
 Best Local Similarity 100.0%; Pred. No. 0.22;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VMAGVGSPPV 10  
 Db 773 VMAGVGSPPV 782  
 RESULT 2  
 TVRTNU  
 A;Title: The neu oncogene encodes an epidermal growth factor receptor-related protein.  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 05-Oct-2004  
 C;Accession: A24562; A61204  
 R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.  
 Nature 319, 226-230, 1986  
 A;Title: The neu oncogene encodes an epidermal growth factor receptor-related protein.  
 A;Reference number: A24562; MUID:96118662; PMID:3945311  
 A;Accession: A24562  
 A;Molecule type: mRNA  
 A;Residues: 1-1260 <BAR>  
 A;Cross-references: UNIPROT:P06494; UNIPARC:UPI00000161883; EMBL:X03362; NID:956745; PIDN  
 R;Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen,  
 Carcinogenesis 12, 1975-1978, 1991  
 A;Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no m  
 2-thiazolyl]formamide or N-methyl-N-nitrosourea.  
 A;Reference number: A61204; MUID:92035293; PMID:1682063  
 A;Accession: A61204  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 637-663, 'V', 665-702 <MAS>  
 A;Cross-references: UNIPARC:UPI00001725C8  
 A;Note: authors translated the codon GCA for residue 25 as Val  
 C;Genetics:  
 A;Gene: neu  
 C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology  
 C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosph  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>  
 F;658-680/Domain: transmembrane #status predicted <TM>  
 F;723-988/Domain: protein kinase homology <KIN>  
 F;731-739/Region: protein kinase ATP-binding motif  
 F;71.191.263.535.576.634/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;651/Binding site: phosphate (Thr) (covalent) #status predicted  
 F;758/Active site: Lys #status predicted

F;882.1227.1253/Binding site: phosphate (Tyr) (covalent) #status predicted  
 Query Match 100.0%; Score 51; DB 1; Length 1250;  
 Best Local Similarity 100.0%; Pred. No. 0.22;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VMAGVGSPPV 10  
 Db 778 VMAGVGSPPV 787  
 RESULT 3  
 I48161  
 P-185 precursor - golden hamster  
 C;Species: Mesocricetus auratus (golden hamster)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Oct-2004  
 C;Accession: I48161  
 R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; Ishikaw  
 Gene 140, 251-255, 1994  
 A;Title: Cloning and activation of the Syrian hamster neu proto-oncogene.  
 A;Reference number: I48161; MUID:94193007; PMID:7908275  
 A;Accession: I48161  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-1254 <RES>  
 A;Cross-references: UNIPROT:Q60553; UNIPARC:UPI000012A111; GB:D16295; NID:G493236; PID  
 C;Genetics:  
 A;Gene: neu  
 C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology  
 C;Keywords: ATP  
 F;718-983/Domain: protein kinase homology <KIN>  
 F;726-734/Region: protein kinase ATP-binding motif  
 Query Match 94.1%; Score 48; DB 2; Length 1254;  
 Best Local Similarity 90.0%; Pred. No. 0.82;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VMAGVGSPPV 10  
 Db 773 VMAGVGSPPV 782

RESULT 4  
 T09037  
 hypothetical protein F26K10.90 - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
 C;Accession: T09037  
 R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Banc  
 submitted to the Protein Sequence Database, June 1999  
 A;Reference number: Z16533  
 A;Accession: T09037  
 A;Molecule type: DNA  
 A;Residues: 1-348 <BEV>  
 A;Cross-references: UNIPROT:Q9M016; UNIPARC:UPI000009E5E1; EMBL:AL049803; GSPDB:GN0006  
 A;Experimental source: cultivar Columbia; BAC clone F26K10  
 C;Genetics:  
 A;Gene: ATSP:F26K10.90  
 A;Map position: 4  
 A;Introns: 120/1  
 C;Superfamily: Arabidopsis thaliana hypothetical protein F26K10.90  
 Query Match 76.5%; Score 39; DB 2; Length 348;  
 Best Local Similarity 70.0%; Pred. No. 12;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 VMAGVGSPPV 10  
 Db 276 VLAGVGEPPV 285  
 RESULT 5  
 A69091

cell division protein FtsZ - Methanobacterium thermoautotrophicum (strain Delta H)  
C;Species: Methanobacterium thermoautotrophicum  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: A69091  
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan, N.; K. S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func  
A;Reference number: A69000; MUID:98037514; PMID:19371463  
A;Accession: A69091  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-381 <MTH>  
A;Cross-references: UNIPROT:O27112; UNIPARC:UPI000012AD23; GB:AE000925; GB:AE000666; NID  
A;Experimental source: strain Delta H  
C;Genetics:  
A;Gene: MTH1676  
A;Start codon: TTG  
C;Superfamily: cell division protein ftsZ  
F;133-139/Region: tubulin/FtsZ GTP/GDP-binding (G-G-G-T-G-[ST]-G) motif

Query Match 74.5%; Score 38; DB 2; Length 381;  
Best Local Similarity 70.0%; Pred. No. 20;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VMAGVSPVY 10  
DB 337 VVAGVSPVY 346  
:::|||||

RESULT 6  
S04987  
SITS-binding protein spl05 - Pacific electric ray  
C;Species: Torpedo californica (Pacific electric ray)  
C;Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004  
C;Accession: S04987; S30070  
R;Jentsch, T.J.; Garcia, A.M.; Lodish, H.F.  
Biochem. J. 261, 155-166, 1989  
A;Title: Primary structure of a novel 4-acetamido-4'-isothiocyanostilbene-2,2'-disulphon  
A;Reference number: S04987; MUID:89374082; PMID:2775201  
A;Accession: S04987  
A;Molecule type: mRNA  
A;Residues: 1-697 <JEN1>  
A;Cross-references: UNIPROT:P19965; UNIPARC:UPI00001714BC; EMBL:X16078; NID:G64403; PIDN  
A;Accession: S30070  
A;Molecule type: protein  
A;Residues: 2-11;435-449, 'X', 451-452, 'X', 454-459;634-649 <JEN2>  
A;Cross-references: UNIPARC:UPI0000174107; UNIPARC:UPI0000174108; UNIPARC:UPI0000174109  
C;Superfamily: SITS-binding protein spl05  
C;Keywords: disulfide bond; glycoprotein; homodimer; transmembrane protein  
F;2-697/Product: SITS-binding protein #status experimental <MAT>  
F;30-50/Domain: transmembrane #status predicted <TM1>  
F;503-521/Domain: transmembrane #status predicted <TM2>  
F;542-562/Domain: transmembrane #status predicted <TM3>  
F;25,112,134,162,386,405,470,568/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match 74.5%; Score 38; DB 1; Length 697;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GVGSPVY 10  
DB 436 GVGSPVY 442  
|||||

RESULT 7  
B95109  
uridylylate kinase [imported] - Streptococcus pneumoniae (strain TIGR4)  
C;Species: Streptococcus pneumoniae  
C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: B95109  
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris  
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A;Reference number: A95000; MUID:21357209; PMID:11463916  
A;Accession: B95109  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-247 <KUR>  
A;Cross-references: UNIPROT:Q97R83; UNIPARC:UPI0000051655; GB:AE005672; PIDN:AAK75067.  
A;Experimental source: strain TIGR4  
C;Genetics:  
A;Gene: SP0944  
C;Superfamily: uridylylate kinase

Query Match 72.5%; Score 37; DB 2; Length 247;  
Best Local Similarity 85.7%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGVGSPY 9  
DB 135 AGIGSPY 141  
|||||

RESULT 8  
E97977  
UMP kinase (BC 2.7.4.-) [imported] - Streptococcus pneumoniae (strain R6)  
C;Species: Streptococcus pneumoniae  
C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C;Accession: E97977  
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;  
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;  
Y. P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.  
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A;Reference number: A97872; MUID:21429245; PMID:11544234  
A;Accession: E97977  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-247 <KUR>  
A;Cross-references: UNIPROT:Q8DQ50; UNIPARC:UPI00000E3531; GB:AE007317; PIDN:AAK99649.  
C;Genetics:  
A;Gene: PyrH  
C;Superfamily: uridylylate kinase  
C;Keywords: phosphotransferase

Query Match 72.5%; Score 37; DB 2; Length 247;  
Best Local Similarity 85.7%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGVGSPY 9  
DB 135 AGIGSPY 141  
|||||

RESULT 9  
F70780  
hypothetical protein Rv0881 - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: F70780  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd,  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: F70780  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA

A;Residues: 1-288 <COL>  
A;Cross-references: UNIPROT:Q10543; UNIPARC:UPI0000139DAD; GB:Z73101; GB:AL123456; NID:9  
A;Experimental source: strain H37RV  
C;Genetics:  
A;Gene: Rv0881  
C;Superfamily: conserved hypothetical protein HI0860

Query Match 72.5%; Score 37; DB 2; Length 288;  
Best Local Similarity 75.0%; Pred. No. 23;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MAGVGSPPY 9  
:|||||  
Db 83 LAGVGAPY 90

RESULT 10  
G90450  
hypothetical protein SS02752 [imported] - Sulfolobus solfataricus  
C;Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C;Accession: G90450  
R;She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.  
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.;  
submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.  
A;Reference number: A99139  
A;Accession: G90450  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-388 <KUR>  
A;Cross-references: UNIPROT:Q97V83; UNIPARC:UPI000006483D; GB:AE006641; NID:gl3816083; F  
C;Genetics:  
A;Gene: SS02752

Query Match 72.5%; Score 37; DB 2; Length 388;  
Best Local Similarity 60.0%; Pred. No. 31;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VMAGVGSPYV 10  
:|||||  
Db 16 IKGGVGITPYV 25

RESULT 11  
D83679  
hypothetical protein BH0236 [imported] - Bacillus halodurans (strain C-125)  
C;Species: Bacillus halodurans  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C;Accession: D83679  
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A;Reference number: A83650; MUID:20512582; PMID:11058132  
A;Accession: D83679  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1020 <STO>  
A;Cross-references: UNIPROT:Q9KG76; UNIPARC:UPI00000C37F3; GB:AP001507; GB:BA000004; NID  
A;Experimental source: strain C-125  
C;Genetics:  
A;Gene: BH0236

Query Match 72.5%; Score 37; DB 2; Length 1020;  
Best Local Similarity 85.7%; Pred. No. 81;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GVGSPYV 10  
:|||||  
Db 177 GVGSPYI 183

RESULT 12  
T35138  
hypothetical protein SC4H8.07c SC4H8.07c - Streptomyces coelicolor  
C;Species: Streptomyces coelicolor  
C;Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
C;Accession: T35138  
R;Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, December 1997  
A;Reference number: Z21569  
A;Accession: T35138  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-66 <HAR>  
A;Cross-references: UNIPROT:O50486; UNIPARC:UPI00000DAB8E; EMBL:AL020958; PIDN:CAA1587  
A;Experimental source: strain A3(2)  
C;Genetics:  
A;Gene: SC0EDB:SC4H8.07c

Query Match 70.6%; Score 36; DB 2; Length 66;  
Best Local Similarity 75.0%; Pred. No. 8.2;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSP 8  
:|||||  
Db 18 VLAGIGSP 25

RESULT 13  
D46177  
enhancer of split locus protein m3 - fruit fly (Drosophila melanogaster)  
N;Alternate names: E(spl)-HLH-m3; helix-loop-helix protein m3  
C;Species: Drosophila melanogaster  
C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: D46177; D38980; S27814; S28449  
R;Delidakis, C.; Artavanis-Tsakonas, S.  
Proc. Natl. Acad. Sci. U.S.A. 89, 8731-8735, 1992  
A;Title: The Enhancer of split [E(spl)] locus of Drosophila encodes seven independent  
A;Reference number: A46177; MUID:92409590; PMID:1528887  
A;Accession: D46177  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-224 <DEL>  
A;Cross-references: UNIPROT:Q01068; UNIPARC:UPI000000118F; EMBL:M96165; NID:g158490; F  
A;Note: sequence extracted from NCBI backbone (NCBIP:114183)  
R;Kunst, E.; Schrons, H.; Grawe, F.; Campos-Ortega, J.A.  
Genetics 132, 505-518, 1992  
A;Title: Seven genes of the Enhancer of split complex of Drosophila melanogaster encod  
A;Reference number: A38980; MUID:93051287; PMID:1427040  
A;Accession: D38980  
A;Molecule type: mRNA  
A;Residues: 1-149,151-173, 'SRR', 177-178,180-224 <KNU>  
A;Cross-references: UNIPARC:UPI0000168C2C; EMBL:X67046; NID:g8073; PIDN:CAA47431.1; PI  
A;Experimental source: strain Oregon R  
C;Genetics:  
A;Gene: FlyBase:HLHm3  
A;Cross-references: FlyBase:FBgn0002609

Query Match 70.6%; Score 36; DB 2; Length 224;  
Best Local Similarity 87.5%; Pred. No. 28;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VMAGVGSP 8  
:|||||  
Db 79 VMAGVGSP 86

RESULT 14  
WMBE4  
UL34 protein - human herpesvirus 1 (strain 17)  
C;Species: human herpesvirus 1  
C;Date: 31-Dec-1989 #sequence\_revision 31-Dec-1989 #text\_change 09-Jul-2004  
C;Accession: G30085  
R;McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Frame, M.C.; Dolan, A.; McNab, D.; Pe

J. Gen. Virol. 69, 1531-1574, 1988  
A;Title: The complete DNA sequence of the long unique region in the genome of herpes sim  
A;Reference number: A30083; MUID:88274327; PMID:2839594  
A;Accession: G30085  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-275 <MCG>  
A;Cross-references: UNIPROT:P10218; UNIPARC:UPI0000137B9E; GB:X14112; NID:G1944536; PIDN  
C;Genetics:  
A;Gene: UL34  
C;Superfamily: varicella-zoster virus gene 24 protein

Query Match 70.6%; Score 36; DB 1; Length 275;  
Best Local Similarity 75.0%; Pred. No. 34;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 MAGVGSPPY 9  
|||:|  
Db 1 MAGLGKPY 8

## RESULT 15

S65829  
hypothetical protein 3 - beet mild yellowing virus  
C;Species: beet mild yellowing virus  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C;Accession: S65829  
R;Guilley, H.; Richards, K.E.; Jonard, G.  
Arch. Virol. 140, 1109-1118, 1995  
A;Title: Nucleotide sequence of beet mild yellowing virus RNA.  
A;Reference number: S65825; MUID:95336315; PMID:7611881  
A;Accession: S65829  
A;Molecule type: genomic RNA  
A;Residues: 1-625 <GUI>  
A;Cross-references: UNIPARC:UPI00001757FF; EMBL:X83110  
A;Experimental source: isolate 21TB  
A;Note: this reading frame extends between two stop codons and does not begin with a sta  
C;Superfamily: potato leaf roll virus RNA-directed RNA polymerase

Query Match 70.6%; Score 36; DB 2; Length 625;  
Best Local Similarity 87.5%; Pred. No. 77;  
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGVGSPYV 10  
|||:|  
Db 273 AGVGSPYV 280

Search completed: April 11, 2006, 19:35:24  
Job time : 40 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 11, 2006, 19:27:40 ; Search time 230 Seconds  
(without alignments)  
30.675 Million cell updates/sec

Title: US-09-277-064-12  
Perfect score: 51  
Sequence: 1 VMAGVSPYV 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	304	Q68KJ7_FELCA	Q68KJ7 felis silve
2	51	100.0	435	Q6ZMM4_HUMAN	Q6ZMM4 homo sapien
3	51	100.0	881	Q8C0E7_MOUSE	Q8C0E7 m mus muscu
4	51	100.0	1255	1 ERBB2_HUMAN	P04626 homo sapien
5	51	100.0	1257	1 ERBB2_RAT	P06494 rattus norv
6	51	100.0	1259	1 ERBB2_CANFA	O18735 canis fami
7	51	100.0	1259	2 Q8K3F9_RAT	Q8K3F9 rattus norv
8	51	100.0	1305	2 Q6ZPE0_MOUSE	Q6ZPE0 mus musculu
9	48	94.1	1254	1 ERBB2_MESAU	Q60553 mesocricetu
10	45	88.2	1275	2 Q5EBY4_BRARE	Q5EBY4 brachydanio
11	43	84.3	519	2 Q4HWH3_GIBZE	Q4HWH3 gibberella
12	42	82.4	270	2 Q4T640_TETNG	Q4T640 tetraodon n
13	41	80.4	286	2 Q5JG55_PYRKO	Q5JG55 pyrococcus
14	40.5	79.4	63	2 Q4HIF2_HUMAN	Q4HIF2 homo sapien
15	40	78.4	65	2 Q4HIF1_HUMAN	Q4HIF1 homo sapien
16	39	76.5	348	2 Q8LFF9_ARATH	Q8LFF9 arabidopsis
17	39	76.5	348	2 Q9M016_ARATH	Q9M016 arabidopsis
18	39	76.5	465	2 Q523R8_MAGGR	Q523R8 magnaporthe
19	39	76.5	535	2 Q4NMC7_9MICC	Q4NMC7 arthrobacte
20	38	74.5	190	2 Q8KUI3_ACTPA	Q8KUI3 actinosyne
21	38	74.5	245	2 Q8DSY1_STRMU	Q8DSY1 streptococc
22	38	74.5	269	2 Q9WMW2_SYNPF	Q9WMW2 synecococc
23	38	74.5	317	2 Q5NOR2_SYNPF	Q5NOR2 synecococc
24	38	74.5	381	1 FTSZ_METH	O27712 methanobact
25	38	74.5	696	1 SP15_TORCA	P19655 torredo cal
26	37	72.5	158	2 Q88IB8_PSEPK	Q88IB8 pseudomonas
27	37	72.5	242	1 PYRH_STRP3	P65939 streptococc
28	37	72.5	242	1 PYRH_STRP6	Q5XDH4 streptococc
29	37	72.5	242	1 PYRH_STRP8	P65940 streptococc
30	37	72.5	242	1 PYRH_STRPV	P65938 streptococc
31	37	72.5	242	2 Q8DY98_STRAS5	Q8DY98 streptococc

Q8E431 streptococc  
Q5M141 streptococc  
Q5M5N0 streptococc  
Q4NGD9 arthrobacte  
Q97Z83 streptococc  
Q8DQ50 streptococc  
Q10543 mycobacteri  
P59968 mycobacteri  
Q8P283 methanosarc  
Q8T886 methanosarc  
Q8TUN5 methanosarc  
Q97V83 sulfolobus  
Q7U456 synecococc  
Q8U3E3 pyrococcus

242 2 Q8E431\_STRAS3  
245 2 Q5M141\_STRT1  
245 2 Q5M5N0\_STRT2  
246 2 Q4NGD9\_9MICC  
247 1 PYRH\_STRPN  
247 1 PYRH\_STRP6  
247 1 Y881\_MYCTU  
288 1 Y905\_MYCBO  
288 1 Y905\_MYCBO  
296 2 Q8P283\_METWA  
296 2 Q8T886\_METAC  
296 2 Q8TUN5\_METAC  
388 2 Q97V83\_SULSO  
389 2 Q7U456\_SYNPX  
408 1 FTSZ2\_PYRFU

## ALIGNMENTS

## RESULT 1

Q68KJ7\_FELCA PRELIMINARY; PRT; 304 AA.  
AC Q68KJ7;  
DT 25-OCT-2004 (TREMELrel. 28, Created)  
DT 25-OCT-2004 (TREMELrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)  
DE HER2 (Fragment).  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;  
OC Felinae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15705889;  
RA De Maria R., Olivero M., Iussich S., Nakaichi M., Murata T.,  
RA Biolatti B., Di Renzo M.P.;  
RT "Spontaneous feline Mammary Carcinoma Is a Model of HER2  
RT Overexpressing Poor Prognosis Human Breast Cancer";  
RL Cancer Res. 65:907-912 (2005).  
DR EMBL; AY685128; AAU01910.1; -; Genomic\_DNA.  
DR SMR; Q68KJ7; 57-304.  
DR GO; GO:0005524; F-ATP binding; IEA.  
DR GO; GO:0004674; F-protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F-protein-tyrosine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR002290; Ser Thr kinase.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR PRINTS; PRO0109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
KW ATP-binding; Kinase; Nucleotide-binding; Transferase.  
FT NON\_TER 1 304  
FT NON\_TER 304 304  
SQ SEQUENCE 304 AA; 33934 MW; 47C0290F4BC020ED CRC64;

Query Match 100.0%; Score 51; DB 2; Length 304;  
Best Local Similarity 100.0%; Pred. No. 0.33;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVSPYV 10  
DB 126 VMAGVSPYV 135

## RESULT 2

Q6ZMM4 HUMAN  
ID Q6ZMM4\_HUMAN PRELIMINARY; PRT; 435 AA.  
AC Q6ZMM4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein FLJ16821.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,  
RA Tanai H., Watanabe S., Ishida S., Ono Y., Hotta T., Watanabe M.,  
RA Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,  
RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,  
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,  
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,  
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK131568; BAD18701.1; -; mRNA.  
DR SMR; Q6ZMM4; 254-434.  
DR GO; GO:0005224; P-ATP binding; IEA.  
DR GO; GO:0005489; F-electron transporter activity; IEA.  
DR GO; GO:0005506; F-iron ion binding; IEA.  
DR GO; GO:0004674; F-protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004713; F-protein-tyrosine kinase activity; IEA.  
DR GO; GO:0004872; F-receptor activity; IEA.  
DR GO; GO:0006118; P-electron transport; IEA.  
DR GO; GO:0006468; P-protein amino acid phosphorylation; IEA.  
DR InterPro; IPR001450; 4Fe4S-ferredoxin.  
DR InterPro; IPR006212; Furin repeat.  
DR InterPro; IPR000719; Prot Kinase.  
DR InterPro; IPR002290; Ser Thr kinase.  
DR InterPro; IPR001245; Tyr\_kinase\_AS.  
DR PRINTS; PR00353; 4FE4SFRDXIN.  
DR PRODOM; PD000001; Prot kinase; 1.  
DR SMART; SM00261; FU\_2.  
DR SMART; SM00220; S\_TKc; 1.  
DR SMART; SM00219; TYR\_Kc; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
KW Kinase; Receptor; Tyrosine-protein kinase.  
SQ SEQUENCE 435 AA; 47891 MW; 1FA846710D31311A CRC64;  
Query Match 100.0%; Score 51; DB 2; Length 435;  
Best Local Similarity 100.0%; Pred. No. 0.46;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VMAGVGSPPV 10  
Db 323 VMAGVGSPPV 332  
RESULT 3  
Q80C07\_MOUSE  
ID Q80C07\_MOUSE PRELIMINARY; PRT; 881 AA.  
AC Q80C07;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Mus musculus 13 days embryo male testis cDNA, RIKEN full-length  
enriched library, clone:603049F08 product:v-erb-b2 erythroblastic  
leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene  
homolog (avian), full insert sequence. (Fragment).  
DE Name=ErbB2;  
GN Mus musculus (Mouse).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukushima Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Mateu Y., Nikaudo I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazarrelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaki S., Inoue K., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Iehikawa T., Ogawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,



RA Chao H.-S., Mason K., Ramyar K.X., Stanley A.M., Gabelli S.B.,  
RA Denney D.W. Jr., Leary D.J.;  
RT "Structure of the extracellular region of HER2 alone and in complex  
RT with the Herceptin Fab.";  
RL Nature 421:756-760(2003).  
RN [12]  
RP VARIANTS VAL-654 AND VAL-655.  
RX MEDLINE=93194196; PubMed=8095488;  
RA Ehsani A., Low J., Wallace R.B., Wu A.M.;  
RT "Characterization of a new allele of the human ERBB2 gene by allele-  
RT specific competition hybridization.";  
RL Genomics 15:426-429(1993).  
CC -!- FUNCTION: Essential component of a neurotrophin-receptor complex,  
CC although neurotrophins do not interact with it alone. GP30 is a  
CC potential ligand for this receptor. Not activated by EGF, TGF-  
CC alpha and amphiregulin.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein  
CC tyrosine phosphate.  
CC -!- SUBUNIT: Heterodimer with each of the other ERBB receptors  
CC (Potential). Interacts with PKRCAP (By similarity). Binds PLXNB1.  
CC Part of a complex with EGFR and either PIK3C2A or PIK3C2B. May  
CC interact with PIK3C2B when phosphorylated on Tyr-1196.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- PTM: Ligand-binding increases phosphorylation on tyrosine residues  
CC (By similarity).  
CC -!- POLYMORPHISM: There are four alleles due to the variations in  
CC positions 654 and 655. Allele B1 (Ile-654/Ile-655) has a frequency  
CC of 0.782; allele B2 (Ile-654/Val-655) has a frequency of 0.206;  
CC allele B3 (Val-654/Val-655) has a frequency of 0.012.  
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor  
CC subfamily.

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the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.

-----  
DR EMBL; M11767; AAA35808.1; -; Genomic DNA.  
DR EMBL; M11761; AAA35808.1; JOINED; Genomic DNA.  
DR EMBL; M11762; AAA35808.1; JOINED; Genomic DNA.  
DR EMBL; M11763; AAA35808.1; JOINED; Genomic DNA.  
DR EMBL; M11764; AAA35808.1; JOINED; Genomic DNA.  
DR EMBL; M11765; AAA35808.1; JOINED; Genomic DNA.  
DR EMBL; M11766; AAA35808.1; JOINED; Genomic DNA.  
DR EMBL; M11730; AAA75493.1; -; mRNA.  
DR EMBL; M12036; AAA35978.1; -; Genomic DNA.  
DR EMBL; AY208911; AAO18082.1; -; Genomic DNA.  
DR EMBL; X03363; CA227060.1; -; mRNA.  
DR EMBL; M16792; AAA58637.1; -; Genomic DNA.  
DR EMBL; M16789; AAA58637.1; JOINED; Genomic DNA.  
DR EMBL; M16790; AAA58637.1; JOINED; Genomic DNA.  
DR EMBL; M16791; AAA58637.1; JOINED; Genomic DNA.  
DR EMBL; L29395; AAA35809.1; -; Genomic DNA.  
DR EMBL; M55667; AAC37531.1; -; Unassigned DNA.  
DR PIR; A24571; A24571.  
DR PDB; 1N8Z; X-ray; C=23-629.  
DR PDB; 1OV6; Model; A=737-1031.  
DR PDB; 1S78; X-ray; A/B=23-646.  
DR Ensemble; ENSG00000141736; Homo sapiens.  
DR HGNC; HGNC:3430; ERBB2.  
DR MIM; 164870; -.  
DR GO; GO:0016021; C:integral to membrane; NAS.  
DR GO; GO:0005886; C:plasma membrane; NAS.  
DR GO; GO:0005006; F:epidermal growth factor receptor activity; NAS.  
DR GO; GO:0043125; F:ErBB-3 class receptor binding; TAS.  
DR GO; GO:0046982; F:protein heterodimerization activity; NAS.  
DR GO; GO:0004716; F:receptor signaling protein tyrosine kinase . . . ; TAS.  
DR GO; GO:0008283; P:cell proliferation; TAS.  
DR GO; GO:0007507; P:heart development; TAS.  
DR GO; GO:0030879; P:mammary gland development; TAS.  
DR GO; GO:0007399; P:neurogenesis; TAS.  
DR GO; GO:0046015; P:phosphoinositide-mediated signaling; NAS.

DR GO; GO:0006458; P:protein amino acid phosphorylation; TAS.  
DR GO; GO:0045785; P:regulation of angiogenesis; NAS.  
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; NAS.  
DR InterPro; IPR000494; EGFR\_L.  
DR InterPro; IPR006211; Furin-like.  
DR InterPro; IPR006212; Furin repeat.  
DR InterPro; IPR000719; Prot\_Kinase.  
DR InterPro; IPR001245; Tyr\_Kinase.  
DR InterPro; IPR008266; Tyr\_Kinase\_AS.  
DR InterPro; IPR004019; YLP\_motif.  
DR Pfam; PF00757; Furin-like; 1.  
DR Pfam; PF01030; Recep\_L\_domain; 2.  
DR Pfam; PF02757; YLP; 2.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_Kinase; 1.  
DR SMART; SM00261; FU; 3.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
KW 3D-structure; ATP-binding; Glycoprotein; Kinase; Multigene family;  
KW Nucleotide-binding; Phosphorylation; Polymorphism; Receptor; Signal;  
KW Transferase; Transmembrane; Tyrosine-protein kinase.  
FT SIGNAL 1 21 Potential.  
FT CHAIN 22 1255 Receptor tyrosine-protein kinase erbB-2.  
FT TOPO\_DOM 22 652 Extracellular (Potential).  
FT TRANSMEM 653 675 Potential.  
FT TOPO\_DOM 676 1255 Cytoplasmic (Potential).  
FT DOMAIN 720 987 Protein kinase.  
FT NP\_BIND 726 734 ATP (By similarity).  
Query Match 100.0%; Score 51; DB 1; Length 1255;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VMAGVGSPYV 10  
DB 773 VMAGVGSPYV 782  
|||||  
RESULT 5  
ERBB2 RAT STANDARD; PRT; 1257 AA.  
ID ERBB2 RAT STANDARD; PRT; 1257 AA.  
AC P06494; Q8P732;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Receptor tyrosine-protein kinase erbB-2 precursor (EC 2.7.1.112)  
DE (p185erbB2) (C-erbB-2) (NEU proto-oncogene) (Epidermal growth factor  
DE receptor-related protein).  
DE Name=Erbb2; Synonyms=Neu;  
DE Rattus norvegicus (Rat).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Neuroblastoma;  
RX MEDLINE=86118662; PubMed=3945311;  
RA Bargmann C.I., Hung M.-C., Weinberg R.A.;  
RT "The neu oncogene encodes an epidermal growth factor receptor-related  
RT protein.";  
RL Nature 319:226-230(1986).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Prostate;  
RG NIH - Mammalian Gene Collection (MGC) project;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE OF 634-699.  
RX MEDLINE=92035293; PubMed=1682063;  
RA Masui T., Mann A.M., Macatee T.L., Garland B.M., Okamura T.,



RN RP NUCLEOTIDE SEQUENCE.  
 RA YOKOTA H.;  
 RT "CDNA cloning of erbB-2 from canine mammary gland."  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Essential component of a neurotrophin-receptor complex,  
 CC although neurotrophins do not interact with it alone. GP30 is a  
 CC potential ligand for this receptor. Not activated by EGF, TGF-  
 CC alpha and amphiregulin (By similarity).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein  
 CC tyrosine phosphate.  
 CC -1- SUBUNIT: Heterodimer with each of the other ERBB receptors  
 CC (Potential). Interacts with PRKABP. Binds PLXNB1. Part of a  
 CC complex with EGFR and either PIK3C2A or PIK3C2B. May interact with  
 CC PIK3C2B when phosphorylated on Tyr-1200 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- PTM: Ligand-binding increases phosphorylation on tyrosine residues  
 CC (By similarity).  
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor  
 CC subfamily.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; AB008451; BAA23127.1; -; mRNA.  
 DR HSSP; P04626; IN8Z.  
 DR SMART; O18735; 23-628.  
 DR Ensembl; ENSCARG00000016351; Canis familiaris.  
 DR InterPro; IPR000494; EGFR\_L.  
 DR InterPro; IPR006211; Furin-like.  
 DR InterPro; IPR006212; Furin repeat.  
 DR InterPro; IPR000719; Prot Kinase.  
 DR InterPro; IPR001245; Tyr\_Pkinase.  
 DR InterPro; IPR008266; Tyr\_Pkinase\_AS.  
 DR Pfam; PF00757; Furin-like; 1.  
 DR Pfam; PF01030; Recep\_L domain; 2.  
 DR Pfam; PF02757; YLP\_2.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00261; FU; 3.  
 DR SMART; SM00219; TyRK; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00111; PROTEIN KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE\_TYR; 1.  
 KW ATP-binding; Glycoprotein; Kinase; Multigene family;  
 KW Nucleotide-binding; Phosphorylation; Receptor; Signal; Transferase;  
 KW Transmembrane; Tyrosine-protein kinase.  
 FT SIGNAL 1 22 Potential.  
 FT CHAIN 23 1259 Receptor tyrosine-protein kinase erbB-2.  
 FT TOPO\_DOM 23 653 Extracellular (Potential).  
 FT TRANSMEM 654 674 Potential.  
 FT TOPO\_DOM 675 1259 Cytoplasmic (Potential).  
 FT DOMAIN 719 986 Protein kinase.  
 FT NP\_BIND 725 733 ATP (By similarity).  
 FT REGION 1199 1201 Interaction with PIK3C2B (By similarity).  
 FT COMBIAS 192 268 Cys-rich.  
 FT ACT\_SITE 1101 1219 By similarity.  
 FT BINDING 752 752 ATP (By similarity).  
 FT MOD\_RES 1138 1138 Phosphotyrosine (by autocatalysis) (By  
 FT MOD\_RES 1200 1200 Phosphotyrosine (Potential).  
 FT MOD\_RES 1252 1252 Phosphotyrosine (by autocatalysis) (By  
 FT similarity).  
 FT CARBOHYD 68 68 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 259 259 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 421 421 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 529 529 N-linked (GlcNAc... ) (Potential).

FT CARBOHYD 570 570 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 628 628 N-linked (GlcNAc... ) (Potential).  
 FT DISULFID 195 204 By similarity.  
 FT DISULFID 199 212 By similarity.  
 FT DISULFID 220 227 By similarity.  
 FT DISULFID 224 235 By similarity.  
 FT DISULFID 236 244 By similarity.  
 FT DISULFID 240 252 By similarity.  
 FT DISULFID 255 264 By similarity.  
 FT DISULFID 268 295 By similarity.  
 FT DISULFID 299 311 By similarity.  
 FT DISULFID 315 331 By similarity.  
 FT DISULFID 334 338 By similarity.  
 FT DISULFID 511 519 By similarity.  
 FT DISULFID 514 527 By similarity.  
 FT DISULFID 530 539 By similarity.  
 FT DISULFID 543 559 By similarity.  
 FT DISULFID 562 575 By similarity.  
 FT DISULFID 566 583 By similarity.  
 FT DISULFID 586 595 By similarity.  
 FT DISULFID 599 622 By similarity.  
 FT DISULFID 625 633 By similarity.  
 FT DISULFID 629 641 By similarity.  
 SQ SEQUENCE 1259 AA; 137991 MW; E37364D49C4ACD46 CRC64;  
 Query Match 100.0%; Score 51; DB 1; Length 1259;  
 Best Local Similarity 100.0%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0;  
 QY 1 VMAGVGSPPV 10  
 DB 772 VMAGVGSPPV 781  
 ID Q8K3F9\_RAT PRELIMINARY; PRT; 1259 AA.  
 AC Q8K3F9\_2 OCT-2002 (TREMELrel. 22, Created)  
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)  
 DE 01-MAR-2004 (TREMELrel. 26, Last annotation update)  
 DE Neu protooncoprotein.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=BDIX;  
 RA Watson P.A., Kim K., Chen K.-S., Gould M.N.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY116182; RAM50093.1; -; mRNA.  
 DR HSSP; P06494; IN8Y.  
 DR SMR; Q8K3F9; 26-633.  
 DR GO; GO:0016020; C-membrane; IEA.  
 DR GO; GO:0005524; F-ATP binding; IEA.  
 DR GO; GO:0005006; P:epidermal growth factor receptor activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; IEA.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR000494; EGFR\_L.  
 DR InterPro; IPR006211; Furin-like.  
 DR InterPro; IPR006212; Furin repeat.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001245; Tyr\_Pkinase.  
 DR InterPro; IPR008266; Tyr\_Pkinase\_AS.  
 DR InterPro; IPR004019; YLP\_motif.  
 DR Pfam; PF00757; Furin-like; 1.  
 DR Pfam; PF01030; Recep\_L domain; 2.  
 DR Pfam; PF02757; YLP; 2.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Prot\_kinase; 1.



DR SMART; SM00261; FU; 4.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
KW ATP-binding; Disease mutation; Glycoprotein; Kinase; Multigene family;  
KW Nucleotide-binding; Phosphorylation; Proto-oncogene; Receptor; Signal;  
KW Transferase; Transmembrane; Tyrosine-protein kinase.  
FT SIGNAL 1 21  
FT CHAIN 22 1254  
FT TOPO\_DOM 22 652  
FT TRANSMEM 653 675  
FT TOPO\_DOM 676 1254  
FT DOMAIN 720 987  
FT NP\_BIND 726 734  
FT REGION 1195 1197  
FT COMPBIAS 158 368  
FT COMPBIAS 472 644  
FT ACT\_SITE 845 845  
FT BINDING 753 753  
FT MOD\_RES 1139 1139  
FT MOD\_RES 1196 1196  
FT MOD\_RES 1247 1247  
FT CARBOHYD 68 68  
FT CARBOHYD 125 125  
FT CARBOHYD 187 187  
FT CARBOHYD 259 259  
FT CARBOHYD 530 530  
FT CARBOHYD 571 571  
FT CARBOHYD 629 629  
FT DISULFID 195 204  
FT DISULFID 199 212  
FT DISULFID 236 244  
FT DISULFID 240 252  
FT DISULFID 255 264  
FT DISULFID 268 295  
FT DISULFID 299 311  
FT DISULFID 315 331  
FT DISULFID 334 338  
FT DISULFID 511 520  
FT DISULFID 515 528  
FT DISULFID 531 540  
FT DISULFID 544 560  
FT DISULFID 563 576  
FT DISULFID 567 584  
FT DISULFID 587 596  
FT DISULFID 600 623  
FT DISULFID 626 634  
FT DISULFID 630 642  
FT VARIANT 658 658  
FT VARIANT 659 659  
SQ SEQUENCE 1254 AA; 138253 MW; 974C3791C21F2BE1 CRC64;  
Query Match 94.1%; Score 48; DB 1; Length 1254;  
Best Local Similarity 90.0%; Pred. No. 4.8;  
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VMAGVGSPPV 10  
DB 773 VMAGLGSPPV 782  
RESULT 10  
QSEBY4\_BRARE PRELIMINARY; PRT; 1275 AA.  
AC QSEBY4;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Erbb2.  
GN Name=erbb2; ORFNames=zgc:63601;

OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15797019;  
RA Lyons D.A., Pogoda H.M., Voas M.G., Woods I.G., Diamond B., Nix R.,  
RA Arana N., Jacobs J., Talbot W.S.;  
RT "erbb3 and erbb2 Are Essential for Schwann Cell Migration and  
RT Myelination in Zebrafish.";  
RL Curr. Biol. 15:513-524(2005).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX Pogoda H.-M., Voas M.G., Talbot W.S.;  
RT "Analysis of a zebrafish erbb2 gene";  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY914799; AAX09341.1; -; mRNA.  
DR ZFIN; ZDB-GENE-031118-121; zgc:63601.  
DR InterPro; IPR000494; EGFR\_L.  
DR InterPro; IPR006211; Furin-like.  
DR InterPro; IPR006212; Furin repeat.  
DR InterPro; IPR000719; Prot Kinase.  
DR InterPro; IPR002290; Ser Thr kinase.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR InterPro; IPR008266; Tyr\_kinase\_AS.  
DR Pfam; PF00757; Furin-like; 1.  
DR Pfam; PF00069; Kinase; 1.  
DR Pfam; PF01030; Recep\_L domain; 2.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00261; FU; 3.  
DR SMART; SM00220; S\_TKc; 1.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
SQ SEQUENCE 1275 AA; 140828 MW; 67462B4F1B68492F CRC64;  
Query Match 88.2%; Score 45; DB 2; Length 1275;  
Best Local Similarity 90.0%; Pred. No. 19;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VMAGVGSPPV 10  
DB 766 VMAGVASPPV 775  
RESULT 11  
Q4HWH3\_GIBZE PRELIMINARY; PRT; 519 AA.  
AC Q4HWH3;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN Gibberella zeae PH-1.  
OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.  
OX NCBI\_TaxID=229533;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=PH-1;  
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,  
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,  
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,  
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearlano K.,  
RA Diaz J.S., Dodge S., Doolley K., Dorris L., Elkins T., Engels R.,  
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,  
RA Gardyna S., Guerre S., Graham L., Grand-Pierre N., Hafez N.,  
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,

RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,  
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,  
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,  
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,  
RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,  
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,  
RA Oliver J., Petersen K., Phunkhang P., Pierre N., Purcell S.,  
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,  
RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,  
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,  
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,  
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,  
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,  
RA Lander E.;  
RT "Fusarium graminearum genome sequence";  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AACW01000446; EAA70307.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 519 AA; 57083 MW; 4B4CE0B4972A2FA9 CRC64;  
Query Match 84.3%; Score 43; DB 2; Length 519;  
Best Local Similarity 70.0%; Pred. No. 19;  
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VMAGVGSPPV 10  
Db 142 VWAGVGAPYI 151  
[1]|||||:  
[1]|||||:  
RESULT 12  
Q4T640\_TETNG  
ID Q4T640\_TETNG PRELIMINARY; PRT; 270 AA.  
AC Q4T640;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Chromosome undetermined SCAP938, whole genome shotgun sequence.  
DE (Fragment).  
DE ORFNames=GSTENG0006492001;  
OS Tetradon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouteau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segreus B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
RA Blomont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,  
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RG Genoscope, Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC EMBL; CAAE01008938; CAF91642.1; -; Genomic\_DNA.  
DR

FT NON TER 1 1  
SQ SEQUENCE 270 AA; 30448 MW; 29P922C1476C58A8 CRC64;  
Query Match 82.4%; Score 42; DB 2; Length 270;  
Best Local Similarity 90.0%; Pred. No. 16;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VMAGVGSPPV 10  
Db 126 VMAGVGSPPV 135  
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[1]|||||:  
RESULT 13  
Q5JGCS\_PYRKO  
ID Q5JGCS\_PYRKO PRELIMINARY; PRT; 286 AA.  
AC Q5JGCS;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Probable fumarate hydratase, alpha subunit.  
DE OrderedLocusNames=TK1965;  
GN Pyrococcus kodakaraensis (Thermococcus kodakaraensis).  
OS Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Thermococcus.  
OX NCBI\_TaxID=69014;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=KOD1;  
RX PubMed=15710748; DOI=10.1101/gr.3003105;  
RA Fukui T., Atomi H., Kanai T., Matsumi R., Fujiwara S., Imanaka T.;  
RT "Complete genome sequence of the hyperthermophilic archaeon  
RT Thermococcus kodakaraensis KOD1 and comparison with Pyrococcus  
RT genomes";  
RL Genome Res. 15:352-363(2005).  
DR EMBL; AP006878; BAD86154.1; -; Genomic\_DNA.  
DR GO; GO:0016829; P:lyase activity; IEA.  
DR InterPro; IPR004646; TtdA\_fuma\_fumb.  
DR Pfam; PF05681; Fumerase; 1.  
DR TIGRFAMs; TIGR00722; ttda\_fuma\_fumb; 1.  
KW Complete proteome.  
SQ SEQUENCE 286 AA; 30729 MW; DA45B901438BC65 CRC64;  
Query Match 80.4%; Score 41; DB 2; Length 286;  
Best Local Similarity 70.0%; Pred. No. 26;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VMAGVGSPPV 10  
Db 71 VKAGIGSPYL 80  
[1]|||||:  
[1]|||||:  
RESULT 14  
Q4H1F2\_HUMAN  
ID Q4H1F2\_HUMAN PRELIMINARY; PRT; 63 AA.  
AC Q4H1F2;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE ERBB2 (Fragment).  
GN Name=ERBB2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Yamanaka S., Sato M., Fujisaki R., Sakurada A., Inoue A., Nukiwa T.,  
RA Kondo T., Horii A.;  
RT "Exploration of siRNA Targeting EGFR as a Candidate for a Novel  
RT Therapeutic Application in Lung Cancer";  
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AB221349; BAE15959.1; -; Genomic\_DNA.  
DR

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FT NON_TER 1
FT NON_TER 63
SQ SEQUENCE 63 AA; 6927 MW; EE62C915FB7B6D6A CRC64;

Query Match 79.4%; Score 40.5; DB 2; Length 63;
Best Local Similarity 90.9%; Pred. No. 7.5;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VMAGV-GSPYV 10
   |||||
Db 4 VMAGVGSPYV 14

RESULT 15
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AC Q4H1F1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE ERBB2 (Fragment).
GN Name=ERBB2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yamanaka S., Sato M., Fujisaki R., Sakurada A., Inoue A., Nukiwa T.,
RA Kondo T., Horii A.;
RT "Exploration of siRNA Targeting EGFR as a Candidate for a Novel
RT Therapeutic Application in Lung Cancer.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB221350; BAE15960.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 65
SQ SEQUENCE 65 AA; 7111 MW; BF169BFB4415620F CRC64;

Query Match 78.4%; Score 40; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSP 8
   |||||
Db 4 VMAGVGSP 11

Search completed: April 11, 2006, 19:34:40
Job time : 233 secs
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OM protein - protein search, using sw model

Run on: April 11, 2006, 19:15:04 ; Search time 184 Seconds  
(without alignments)  
23.879 Million cell updates/sec

Title: US-09-277-064-12

Perfect score: 51

Sequence: 1 VMAGVSPV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 556551

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 21.\*

- 1: geneseq1980s.\*
- 2: geneseq1980s.\*
- 3: geneseq2000s.\*
- 4: geneseq2001s.\*
- 5: geneseq2002s.\*
- 6: geneseq2003as.\*
- 7: geneseq2003bs.\*
- 8: geneseq2004s.\*
- 9: geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	2 AAR61525	Aar61525 Peptide f
2	51	100.0	10	2 AAR97508	Aar97508 Cytotoxic
3	51	100.0	10	2 AAW36826	Aaw36826 Immunogen
4	51	100.0	10	2 AAW70071	Aaw70071 HER-2/neu
5	51	100.0	10	2 AAW77132	Aaw77132 HER-2/neu
6	51	100.0	10	4 AAB99690	Aab99690 HLA A2 bi
7	51	100.0	10	4 AAG89003	Aag89003 HER2/neu
8	51	100.0	10	4 AAG88772	Aag88772 HER2/neu
9	51	100.0	10	5 AAB76755	Abb76755 Tumour an
10	51	100.0	10	5 AAE26800	Aae26800 Human HLA
11	51	100.0	10	5 AEA36306	Aea36306 Human HER
12	51	100.0	10	6 ABU63012	Abu63012 Human Her
13	51	100.0	10	8 AD97756	Ad97756 Immunogen
14	51	100.0	10	8 ADM12647	Adm12647 MHC class
15	51	100.0	10	8 ADO38880	Ado38880 Human Her
16	51	100.0	10	8 ADP79761	Adp79761 Human HLA
17	47	92.2	9	2 AAY46001	Aay46001 Immunogen
18	47	92.2	9	2 AAY46413	Aay46413 Immunogen
19	47	92.2	9	2 AAY46478	Aay46478 Immunogen
20	47	92.2	9	4 AAG88305	Aag88305 HER2/NEU
21	47	92.2	9	4 AAE12134	Aae12134 Human HLA
22	47	92.2	9	8 ADP79931	Adp79931 Human HLA
23	47	92.2	10	2 AAY37958	Aay37958 Human cER
24	47	92.2	10	2 AAY45527	Aay45527 Immunogen

25	41	80.4	9	4 AAG88941	Aag88941 HER2/neu
26	41	80.4	9	7 ADG38697	Adg38697 Human Her
27	41	80.4	9	7 ADW30548	Adw30548 HLA bindi
28	41	80.4	9	7 ADW30664	Adw30664 HLA bindi
29	41	80.4	9	8 ADP79932	Adp79932 Human HLA
30	40	78.4	9	4 AAG88321	Aag88321 HER2/NEU
31	32	62.7	9	4 AAG88503	Aag88503 HER2/NEU
32	29	56.9	8	4 AAM23398	Aam23398 HIV pepti
33	29	56.9	9	2 AAW30834	Aaw30834 TRP-2 der
34	29	56.9	9	4 AAM23323	Aam23323 HIV pepti
35	29	56.9	9	4 ABP14007	Abp14007 HIV A02 s
36	29	56.9	9	4 ABP19510	Abp19510 HIV B62 s
37	29	56.9	10	4 ABP14013	Abp14013 HIV A02 s
38	29	56.9	10	4 ABP18334	Abp18334 HIV B58 s
39	29	56.9	10	4 ABP16406	Abp16406 HIV A24 s
40	29	56.9	10	7 ADN14184	Adn14184 HIV B cel
41	29	56.9	10	8 ADN64625	Adn64625 HLA bindi
42	29	56.9	10	8 ADP80235	Adp80235 Human HLA
43	28	54.9	8	4 AAM22702	Aam22702 HIV pepti
44	28	54.9	8	4 AAM22701	Aam22701 HIV pepti
45	27	52.9	10	4 AAG93812	Aag93812 Human com

#### ALIGNMENTS

#### RESULT 1

AAR61525

ID AAR61525 standard; peptide; 10 AA.

XX AAR61525;

XX 25-MAR-2003 (revised)

DT 11-MAY-1995 (first entry)

XX Peptide fragment (1.0738) of c-ERB2 binds HLA-A2.1.

XX antigen; epitope; immunogenic target protein; PSA; HBVc; HBVc; HIV1;

KW plasma specific antigen; hepatitis B virus; Epstein Barr; MAGE-1;

KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1;

KW melanoma antigen-1; core antigen; surface antigen;

KW pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;

KW MHC class I molecule; major histocompatibility complex; HLA-A2.1; 9mer;

KW 10mer; anchor; human leukocyte antigen.

XX Homo sapiens.

OS WO9420127-A1.

XX 15-SEP-1994

PD 04-MAR-1994; 94WO-US002353.

XX 05-MAR-1993; 93US-00027146.

XX 04-JUN-1993; 93US-00073205.

XX 29-NOV-1993; 93US-00159184.

XX (CYTE-) CYTEL CORP.

PA Grey HM, Sette A, Sidney J, Kast W;

XX WPI; 1994-302678/37.

XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for

PT treatment or prophylaxis of cancer, virus infection or autoimmune

XX diseases.

XX Example 5; Page 108; 138pp; English.

XX AAR59496-R61666 are immunogenic 10mer peptides that contain a HLA-A2.1

CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity

CC of at least 1% as compared to a reference peptide (AAR71293). AAR61525

CC has an IC50 of 0.018 and the sequence occurs at position 773 in the human

CC c-ERB2 gene product. Peptides of the invention can induce cytotoxic T  
 CC lymphocytes which can react with target cells. They can be used for the  
 CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma, etc.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 51; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VMAGVGSPYV 10  
 DB 1 VMAGVGSPYV 10  
 |||||  
 |||||

RESULT 2  
 AAR97508  
 ID AAR97508 standard; peptide; 10 AA.  
 AC  
 AC AAR97508;  
 DT 11-FEB-1997 (first entry)  
 XX Cytotoxic T lymphocyte-activating Her-2/Neu-specific peptide.  
 DE p53; Her-2; Neu; aa; amino acid; CTL; cytotoxic T lymphocyte; target;  
 KW malignant cell; antigenic; vaccine; immunisation; activation.  
 XX Homo sapiens.  
 OS WO9618409-A1.  
 PN 20-JUN-1996.  
 PD 14-DEC-1995; 95WO-US016415.  
 PF 14-DEC-1994; 94US-00355558.  
 PR (SCRI ) SCRIPPS RES INST.  
 XX Sherman LA;  
 PI WPI; 1996-300385/30.  
 XX In vivo activation of tumour-specific cytotoxic T lymphocytes - by  
 PT contacting with polypeptide(s) derived from human p53 or Her-2/Neu  
 PT proteins.  
 XX Claim 5; Page 124; 158pp; English.  
 PS AAR97508 is a peptide capable of activating cytotoxic T lymphocytes  
 CC (CTLs) which specifically target malignant cells. The peptide corresponds  
 CC to amino acids 773-782 of human Her-2/Neu protein. CTL-activating  
 CC peptides can be used in a vaccine for protecting against tumour cell  
 CC formation. CTLs activated by the peptides will lyse tumour cells  
 CC displaying specific peptides. Antibodies against CTL-activating peptides  
 CC are useful for the identification of other similar compounds which may be  
 CC useful for treating cancer or virally-infected cells, or for diagnosis.  
 CC The peptide and vaccines produced provide immunity to a high percentage  
 CC of different ethnic groups, i.e. those with different HLA alleles  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 51; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VMAGVGSPYV 10  
 DB 1 VMAGVGSPYV 10  
 |||||  
 |||||

RESULT 3  
 AAW36826  
 ID AAW36826 standard; peptide; 10 AA.  
 XX  
 AC AAW36826;  
 DT 23-MAR-1998 (first entry)  
 XX Immunogenic peptide H7 based on the human Her-2/neu protein.  
 DE Her-2/neu protein; human leukocyte antigen A2.1; HLA;  
 KW cytotoxic T lymphocyte; CTL; immune response; tumour-associated antigen;  
 KW T-cell receptor; TCR; tumour treatment.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX WO9732603-A1.  
 PN 12-SEP-1997.  
 PD 05-MAR-1997; 97WO-US003611.  
 PF 05-MAR-1996; 96US-0012845P.  
 PR (SCRI ) SCRIPPS RES INST.  
 XX Sherman LA, Lustgarten J;  
 PI WPI; 1997-470496/43.  
 XX Nucleic acid encoding variable regions of HLA-restricted non-human T cell  
 PT receptor specific for tumour antigen - used to identify tumour antigens  
 PT and for tumour therapy.  
 XX  
 PS Example 1; Page 9; 34pp; English.  
 XX Synthetic peptides AAW36824-40 are based on the sequence of the human Her  
 CC -2/neu protein, wherein each sequence contains the anchor motif for human  
 CC leukocyte antigen (HLA) A2.1. The present peptide is based on positions  
 CC 773-782. The ability of these peptides to inhibit the binding of an  
 CC influenza virus matrix protein peptide M1 to HLA A2.1 was measured by  
 CC inhibition of lysis by an M1 specific, HLA A2.1 restricted, cytotoxic T  
 CC lymphocyte (CTL) clone. The present protein showed 55% inhibition. The  
 CC peptides were also tested for their ability to elicit an immune response  
 CC in vivo. However, only H3 (AAW36824) and H7 (AAW36826) were able to do  
 CC this. H3 and H7 peptides are tumour-associated antigens, and were used to  
 CC immunize a transgenic, non-human vertebrate (that has been modified to  
 CC express at least one HLA antigen), so that the animal produces CTL which  
 CC displays HLA-restricted T-cell receptor (TCR) specificity for the  
 CC antigen. Nucleic acid encoding variable regions of the alpha and beta  
 CC chains of such TCRs can be amplified from CTUs produced in the above  
 CC manner. Cells expressing recombinant TCR are used to identify antigens  
 CC associated with a tumour and to treat tumours in humans. Transgenic mice  
 CC are a more convenient source of CTL than the tumour-infiltrating  
 CC lymphocytes previously used. TCR can be humanised to reduce side-  
 CC reactions and short peptide derivatives of TCR are more economical to  
 CC produce than TCR itself, particularly when expressed as a single-chain  
 CC molecule rather than as a dimer  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 51; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VMAGVGSPYV 10  
 DB 1 VMAGVGSPYV 10  
 |||||  
 |||||

RESULT 4  
 AAW70071



PR 13-DEC-1999; 99US-0170448P.  
 PR 05-APR-2000; 2000US-00543608.  
 PR 30-MAY-2000; 2000US-00583200.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Fikes J, Sette A, Sidney J, Southwood S, Celis E, Keogh E;  
 PI Chesnut R;  
 XX  
 XX WPI; 2001-381489/40.  
 XX  
 XX Compositions for use in a vaccine for treating, e.g., breast, lung and  
 PT colon cancer comprises at least one peptide that comprises an isolated  
 PT epitope of a tumor-associated antigen.  
 XX  
 PS Claim 1; Page 76; 86pp; English.  
 XX  
 XX The present invention describes a composition (I) comprising at least one  
 CC peptide that comprises an isolated, prepared epitope consisting of a  
 CC sequence selected from 25 short amino acid sequences given in AAB99680 to  
 CC AAB99704. Also described are: (1) a composition (II) comprising one or  
 CC more peptides, and further comprising at least two epitopes selected from  
 CC the 25 short amino acid sequences (as above), where each of the one or  
 CC more peptides comprise less than 50 contiguous amino acids that have 100%  
 CC identity with a native peptide sequence; and (2) a vaccine composition  
 CC (III) comprising an epitope selected from the 25 short amino acid  
 CC sequences (as above) and a pharmaceutical excipient. (I) has cytostatic  
 CC and immunomodulatory activities and can be used in vaccine production and  
 CC immunotherapy. The peptide epitope compositions (I)-(II) are useful for  
 CC monitoring an immune response to a tumor associated antigen or when one  
 CC or more peptides are combined to create a vaccine (III) that stimulates  
 CC the cellular arm of the immune system. In particular, the vaccine  
 CC mediates immune responses against tumors in individuals who bear an  
 CC allele of the human leukocyte antigen (HLA)-A2 supertype and improve the  
 CC standard of care for patients being treated for breast, colon, or lung  
 CC cancer  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
 |||||  
 DB 1 VMAGVGSPPV 10

RESULT 7  
 AAG89003  
 ID AAG89003 standard; peptide; 10 AA.  
 XX  
 AC AAG89003;  
 XX  
 DT 11-SEP-2001 (first entry)  
 XX  
 DE HER2/neu epitope HLA-A2 supermotif-bearing peptide #16.  
 XX  
 KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
 KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
 KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200141787-A1.  
 XX  
 PD 14-JUN-2001.  
 XX  
 XX 11-DEC-2000; 2000WO-US033591.  
 PF  
 PR 10-DEC-1999; 99US-00458299.  
 XX

PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
 PI Keogh E;  
 XX  
 XX WPI; 2001-374995/39.  
 XX  
 XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
 PT cellular immune responses for the prevention and treatment of cancer.  
 PT  
 XX  
 PS Claim 1; Page 189; 199pp; English.  
 XX  
 XX The present invention describes isolated prepared HER2/neu epitopes (I).  
 CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
 CC culture in vitro and binds to a complex of an epitope (I), bound to a  
 CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
 CC and a second epitope and the peptide is less than 50 contiguous amino  
 CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
 CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
 CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
 CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
 CC immunostimulant activities, and can be used in vaccines. (I), (II) and  
 CC (III) are useful for inducing cellular immune responses for the  
 CC prevention or treatment of cancer. (I) and (II) are useful for  
 CC monitoring or evaluating an immune response to a tumour-associated  
 CC antigen when incubated with a T lymphocyte sample from a patient and  
 CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
 CC based vaccines mean that immunosuppressive epitopes that may be present  
 CC in whole antigens may be avoided. Selected epitopes may be combined to  
 CC enhance immunogenicity. The possible pathological side effects caused by  
 CC infectious agents or whole protein antigen is eliminated. The vaccine  
 CC provides the ability to direct and focus an immune response to multiple  
 CC selected antigens from the same pathogen. Epitope-based anti-tumour  
 CC vaccines provides the opportunity to combine epitopes derived from  
 CC multiple tumour-associated molecules addressing the problem of tumour-  
 CC tumour variability and reducing the likelihood of tumour escape due to  
 CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
 CC the exemplification of the present invention  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
 |||||  
 DB 1 VMAGVGSPPV 10

RESULT 8  
 AAG88772  
 ID AAG88772 standard; peptide; 10 AA.  
 XX  
 AC AAG88772;  
 XX  
 DT 11-SEP-2001 (first entry)  
 XX  
 DE HER2/neu A2 supermotif crossbinding peptide #16.  
 XX  
 KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;  
 KW immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;  
 KW tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200141787-A1.  
 XX  
 PD 14-JUN-2001.  
 XX  
 XX 11-DEC-2000; 2000WO-US033591.  
 PF  
 XX

PR 10-DEC-1999; 99US-00458299.  
 XX (EPIM-) EPIMUNE INC.  
 XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
 PI Keogh E;  
 XX WPI; 2001-374995/39.  
 DR An isolated prepared HER2/neu epitope useful in a vaccine for inducing  
 XX cellular immune responses for the prevention and treatment of cancer.  
 PT Example 2; Page 179; 199pp; English.  
 PS The present invention describes isolated prepared HER2/neu epitopes (I).  
 XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is  
 CC culture in vitro and binds to a complex of an epitope (I), bound to a  
 CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)  
 CC and a second epitope and the peptide is less than 50 contiguous amino  
 CC acids that have 100% identity with a native peptide sequence of HER2/neu;  
 CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical  
 CC excipient; (4) an isolated nucleic acid encoding a peptide comprising (I)  
 CC ; and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and  
 CC immunostimulant activities, and can be used in vaccines. (II), (III) and  
 CC (III) are useful for inducing cellular immune responses for the  
 CC prevention and treatment of cancer. (I) and (II) are useful for  
 CC monitoring or evaluating an immune response to a tumour-associated  
 CC antigen when incubated with a T lymphocyte sample from a patient and  
 CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope  
 CC based vaccines mean that immunosuppressive epitopes that may be present  
 CC in whole antigens may be avoided. Selected epitopes may be combined to  
 CC enhance immunogenicity. The possible pathological side effects caused by  
 CC infectious agents or whole protein antigen is eliminated. The vaccine  
 CC provides the ability to direct and focus an immune response to multiple  
 CC selected antigens from the same pathogen. Epitope-based anti-tumour  
 CC vaccines provides the opportunity to combine epitopes derived from  
 CC multiple tumour-associated molecules addressing the problem of tumour-  
 CC tumour variability and reducing the likelihood of tumour escape due to  
 CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in  
 CC the exemplification of the present invention  
 XX Sequence 10 AA;  
 SQ Query Match 100.0%; Score 51; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VMAGVGSPTV 10  
 DB 1 VMAGVGSPTV 10  
 RESULT 9  
 ABB76755  
 ID ABB76755 standard; peptide; 10 AA.  
 AC ABB76755;  
 XX 31-MAY-2002 (first entry)  
 DT Tumour antigen epitope HER-2/neu 773 presented by HLA A2.1.  
 DE Antiviral; anti-HIV; cytostatic; epitope; HLA A2.1;  
 XX human leukocyte antigen; immunotherapy; cancer; viral infection; vaccine.  
 KW Unidentified.  
 XX FR2812087-A1.  
 XX 25-JAN-2002.  
 XX 21-JUL-2000; 2000FR-00009591.

PR 21-JUL-2000; 2000FR-00009591.  
 XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX Kosmatopoulos K, Tourdot S, Scardino A, Gross DA;  
 PI WPI; 2002-189846/25.  
 DR Identifying subdominant or cryptic epitopes, useful in immunotherapy of  
 XX cancer and viral infection, comprises testing modified, non-immunogenic  
 PT peptides for induction of cytotoxic T cells.  
 PT Example 1; Page 12; 62pp; French.  
 PS The present invention relates to subdominant/cryptic epitopes that are  
 CC presented by HLA (human leukocyte antigen) Class I molecule A2.1. The  
 CC epitopes or chimeric polypeptides containing them and nucleic acid  
 CC encoding them are useful for preventative or curative immunotherapy of  
 CC cancer and viral infections, particularly where used as vaccines. The  
 CC present peptide was used to illustrate the invention  
 XX Sequence 10 AA;  
 SQ Query Match 100.0%; Score 51; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VMAGVGSPTV 10  
 DB 1 VMAGVGSPTV 10  
 RESULT 10  
 AAE26800  
 ID AAE26800 standard; peptide; 10 AA.  
 AC AAE26800;  
 XX 13-DEC-2002 (first entry)  
 DT Human HLA-A2.1 restricted HER-2/neu peptide epitope #6.  
 XX Human; cancer; breast cancer; ovarian cancer; melanoma; cell therapy;  
 KW epitope; human leukocyte antigen; HLA-A2.1.  
 XX Homo sapiens.  
 OS WO200265992-A2.  
 PN 29-AUG-2002.  
 PD 19-FEB-2002; 2002WO-US005748.  
 PF 20-FEB-2001; 2001US-0270252P.  
 PR (ORTH ) ORTHO-MCNEIL PHARM INC.  
 PA Degraw J, Moriarty A, Leturcq DJ, Jackson MR, Peterson PA;  
 PI Heiskala M;  
 PI WPI; 2002-667033/71.  
 DR Treating a subject with cancer comprises combining the CD-8 cells, which  
 XX are stimulated with non-naturally occurring antigen-presenting cell line,  
 PT with adherent blood monocytes and inoculating the subject with CD8+  
 PT suspension.  
 XX Example 2; Page 92; 99pp; English.  
 PS The invention relates to a method of treating a subject with cancer. The  
 XX method involves combining the CD8 cells, which are stimulated with non  
 CC naturally occurring antigen-presenting cell (mAPC) line, with adherent  
 CC blood monocytes and inoculating the subject with CD8+ suspension. The

CC method is useful for treating cancer e.g. ovarian cancer, breast cancer  
CC and melanoma etc. It is also useful in cell therapy. The present sequence  
CC is human leukocyte antigen A2 (HLA-A2).1 restricted peptide epitope used  
CC to treat breast and ovarian cancer  
XX  
SQ

Sequence 10 AA;

Query Match 100.0%; Score 51; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPIV 10

DB 1 VMAGVGSPIV 10

RESULT 11  
AEA36306  
ID AEA36306 standard; peptide; 10 AA.

XX AEA36306;

XX 11-AUG-2005 (first entry)

XX Human HER-2/neu 773-782 cytotoxic T-lymphocyte epitope peptide.

XX viral infection; virucide; cytostatic; tumor; neoplasm; cell therapy;  
KW antigen; HER-2/neu.

XX Homo sapiens.

XX JP2005139118-A.

XX 02-JUN-2005.

XX 07-NOV-2003; 2003JP-00377653.

XX 20-FEB-2001; 2001US-0270252P.

XX (ORTH ) ORTHO-MCNEIL PHARM INC.

XX Leturco DJ, Moriarty AM, Jackson MR, Peterson PA, Richards JM;

XX WPI; 2002-667033/71.

XX Treating a subject with cancer comprises combining the CD-8 cells, which  
PT are stimulated with non-naturally occurring antigen-presenting cell line,  
PT with adherent blood monocytes and inoculating the subject with CD8+  
PT suspension.

XX Example 3; SEQ ID NO 16; 65pp; Japanese.

XX The invention relates to a novel method for treating viral infection in a  
CC subject. The method comprises preparing an antigen presentation cell  
CC lineage (mNAPC), collecting CD8+ cells from the subject, stimulating CD8+  
CC cells using the mNAPC, culturing CD8+ cells in the presence of  
CC interleukin-2 (IL-2) and/or IL-7, mixing peripheral blood monocytes from  
CC the subject, subjecting the components to gamma irradiation, combining  
CC the CD8+ cells with adhesive peripheral blood monocytes and inoculating  
CC the CD8+ suspended solid to the subject. The method of the invention  
CC demonstrates virucide and cytostatic activities and may be useful for  
CC treating a viral infection or tumor in a subject via cell therapy. The  
CC current sequence is that of a human HER-2/neu cytotoxic T-lymphocyte  
CC epitope peptide of the invention which was incorporated into a Drosophila  
CC antigen presenting cell.

XX Sequence 10 AA;

Query Match 100.0%; Score 51; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPIV 10

DB 1 VMAGVGSPIV 10

RESULT 12

ABU63012  
ID ABU63012 standard; peptide; 10 AA.

XX ABU63012;

XX 16-SEP-2003 (first entry)

XX Human Her-2/Neu-derived CTL epitope HER-7.

XX CTL; cytotoxic C lymphocyte; epitope; p53; cytostatic; anti-tumour;  
KW virucide; immunosuppressive; vaccine; human; immune response;  
KW tumour-associated antigen; cancer; tumour; neoplasm; viral infection;  
KW retroviral infection; autoimmune response; Her-2; Neu.

XX Homo sapiens.

XX US2003064916-A1.

XX 03-APR-2003.

XX 26-MAR-1999; 99US-00277064.

XX 08-AUG-1997; 97US-00860232.

XX (SHER/) SHERMAN L A.

XX Sherman LA;

XX WPI; 2003-512514/48.

XX Novel polypeptide useful for activating cytotoxic T lymphocytes in vivo  
PT which are useful in the diagnosis and treatment of variety of disease  
PT conditions such as cancer, tumors, and neoplasia.

XX Claim 5; Page 52; 77pp; English.

XX The invention relates to a polypeptide capable of specifically activating  
CC cytotoxic T lymphocytes (CTLs) in vivo which can then specifically target  
CC malignant cells or having substantial homology with a CTL epitope, or  
CC its sequential subsets. Also included are a population of specific  
CC cytotoxic T cells capable of lysing tumour cells displaying a specific  
CC peptide, a vaccine comprising an immunogenically effective amount of CTL-  
CC stimulating peptide, generating activated CTL cells in vivo, generating  
CC CTL cells that will target a specific population of cells, specifically  
CC killing target cells in an individual using specific, activated CTLs,  
CC provoking an immune response to a tumour-associated antigen, identifying  
CC specific CTLs responsive to a specific T cell epitope, detecting specific  
CC CTLs having receptors capable of binding a specific T cell epitope in a  
CC tissue sample, detecting anti-p53 antibodies in an individual, an  
CC antibody molecule that immunoreacts with the polypeptide and a hybridoma  
CC capable of secreting the above antibodies. The methods are useful for  
CC specifically killing target cells in an individual using specific.  
CC activated CTLs and the polypeptide is useful for provoking an immune  
CC response to a tumour-associated antigen in mammal and the reaction occurs  
CC in vitro. The CTL epitope peptide is useful for activating CTLs in vivo  
CC with specificity for particular antigenic peptides, and these activated  
CC CTLs are useful in the diagnosis and treatment of variety of disease  
CC conditions such as cancer, tumours, neoplasia, viral and retroviral  
CC infections, and autoimmune response. The present sequence is a CTL  
CC epitope of the invention derived from the tumour associated antigen Her-  
CC 2/Neu

XX Sequence 10 AA;

Query Match 100.0%; Score 51; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVSPYV 10  
 DB 1 VMAGVSPYV 10

RESULT 13  
 ADE97756  
 ID ADE97756 standard; peptide; 10 AA.  
 AC ADE97756;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Immunogenic HLA-A2.1 binding peptide #238.  
 XX  
 KW cytostatic; anti-inflammatory; hepatotropic; virucide; anti-HIV;  
 KW nephrotropic; neuroprotective; antiarthritic; antirheumatic;  
 KW immunosuppressive; dermatological; muscular; nephrotropic; thyromimetic;  
 KW haemostatic; antithyroid; antianaemic; anabolic; hypertensive;  
 KW immunogenic peptide composition; immune response; prostate cancer;  
 KW hepatitis B; hepatitis C; AIDS; renal carcinoma; cervical carcinoma;  
 KW lymphoma; cytomegalovirus; CMV; condyloma acuminatum;  
 KW autoimmune associated disorder; multiple sclerosis; rheumatoid arthritis;  
 KW Sjogren syndrome; scleroderma; polymyositis; dermatomyositis;  
 KW systemic lupus erythematosus; juvenile rheumatoid arthritis;  
 KW ankylosing spondylitis; myasthenia gravis; MG; bullous pemphigoid;  
 KW pemphigus; glomerulonephritis; Goodpasture's disease;  
 KW autoimmune haemolytic anaemia; Hashimoto's disease; pernicious anaemia;  
 KW idiopathic thrombocytopenic purpura; Grave's disease; Addison's disease;  
 KW human leukocyte antigen A2.1; HLA A2.1;  
 KW immunogenic HLA-A2.1 binding peptide.  
 XX  
 OS Synthetic.  
 XX  
 XX US2003185822-A1.  
 XX  
 XX 02-OCT-2003.  
 XX  
 XX 03-APR-2002; 2002US-00116557.  
 XX  
 XX 05-MAR-1993; 93US-00027146.  
 PR 04-JUN-1993; 93US-00073205.  
 PR 29-NOV-1993; 93US-00159184.  
 PR 02-DEC-1994; 94US-00349177.  
 XX  
 XX (GREY/) GREY H M.  
 PA (SETT/) SETTE A.  
 PA (SIDN/) SIDNEY J.  
 XX  
 PI Grey HM, Sette A, Sidney J;  
 XX  
 DR WPI; 2004-041186/04.  
 XX  
 PT Immunogenic peptide composition for preventing, treating or diagnosing  
 PT pathological states, e.g. prostate cancer, hepatitis B and C. Acquired  
 PT Immunodeficiency Syndrome, and renal carcinoma, includes conserved  
 PT residues at specified positions.  
 XX  
 XX Example 11; Page 25; 38pp; English.  
 XX  
 CC The invention describes an immunogenic peptide composition comprising 9  
 CC residues including a first conserved residue at a second position from N-  
 CC terminus, and a second conserved residue at C-terminal position. The  
 CC inventive peptide composition is used to elicit an immune response  
 CC against a desired antigen for preventing, treating or diagnosing  
 CC pathological states, e.g. prostate cancer, hepatitis B, hepatitis C,  
 CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, cytomegalovirus  
 CC (CMV), and condyloma acuminatum. It is also used to treat autoimmune  
 CC associated disorders, e.g. multiple sclerosis, rheumatoid arthritis,  
 CC Sjogren syndrome, scleroderma, polymyositis, dermatomyositis, systemic  
 CC lupus erythematosus, juvenile rheumatoid arthritis, ankylosing  
 CC spondylitis, myasthenia gravis (MG), bullous pemphigoid, pemphigus,  
 CC glomerulonephritis, Goodpasture's syndrome, autoimmune hemolytic anemia,

CC Hashimoto's disease, pernicious anaemia, idiopathic thrombocytopenic  
 CC purpura, Grave's disease, and Addison's disease. The invention defines  
 CC positions within a motif enabling the selection of the peptides, which  
 CC will bind efficiently to human leukocyte antigen (HLA) A2.1. This is the  
 CC amino acid sequence of an immunogenic HLA-A2.1 binding peptide.  
 XX  
 XX Sequence 10 AA;  
 QY Query Match 100.0%; Score 51; DB 8; Length 10;  
 DB Best Local Similarity 100.0%; Pred. No. 0.013;  
 Mismatches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VMAGVSPYV 10  
 DB 1 VMAGVSPYV 10

RESULT 14  
 ADM12647  
 ID ADM12647 standard; peptide; 10 AA.  
 AC ADM12647;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE MHC class I epitope of human Her-2/neu, 16-6-9.  
 XX  
 KW antigen presentation enhancing hybrid polypeptide; mammalian Ii-Key;  
 KW MHC class II; antibacterial; virucide; fungicide; antirheumatic;  
 KW antiarthritic; neuroprotective; dermatological; immunosuppressive;  
 KW antinflammatory; antidiabetic; antithyroid; immune;  
 KW rheumatoid arthritis; multiple sclerosis; lupus erythematosus;  
 KW diabetes mellitus; myasthenia gravis; autoimmune thyroiditis;  
 KW scleroderma; dermatomyositis; pemphigus.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2003235594-A1.  
 XX  
 XX 25-DEC-2003.  
 XX  
 XX 17-SEP-2002; 2002US-00245871.  
 PR 14-SEP-1999; 99US-00396813.  
 PR 17-JUL-2002; 2002US-00197000.  
 XX  
 XX (ANTI-) ANTIGEN EXPRESS INC.  
 PA  
 XX Humphreys R, Xu M;  
 XX  
 XX WPI; 2004-070554/07.  
 XX  
 PT Novel Ii-Key/antigen presentation enhancing hybrid polypeptide, useful  
 PT for treating infections, rheumatoid arthritis, multiple sclerosis, lupus  
 PT erythematosus and diabetes mellitus.  
 XX  
 XX Example 16; Page 55; 87pp; English.  
 XX  
 CC The invention relates to a novel antigen presentation enhancing hybrid  
 CC polypeptide. The novel polypeptide has an N-terminal element consisting  
 CC of 4-16 residues of a mammalian Ii-Key peptide and its non-N-terminal  
 CC deletion modifications, a chemical structure covalently linking the N-  
 CC terminal element to an MHC class II-presented epitope of a C-terminal  
 CC element. The C-terminal element comprises an antigenic epitope, which  
 CC binds to an antigenic peptide binding site of an MHC class II molecule.  
 CC The antigen presentation enhancing hybrid polypeptide has the following  
 CC activities: antibacterial, virucide, fungicide, antirheumatic,  
 CC antiarthritic, neuroprotective, dermatological, immunosuppressive,  
 CC antinflammatory, antidiabetic, and antithyroid. The antigen presentation  
 CC enhancing hybrid polypeptide is useful for modulating the immune response  
 CC in an individual and for treating infections (such as bacteria, virus,  
 CC parasite and fungus), rheumatoid arthritis, multiple sclerosis, lupus  
 CC erythematosus, diabetes mellitus, myasthenia gravis, autoimmune

CC thyroiditis, scleroderma, dermatomyositis and pemphigus. This sequence  
 CC represents a mammalian II key related peptide epitope of the invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 51; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VMAGVGSPYV 10  
 Db 1 VMAGVGSPYV 10  
 |||||  
 RESULT 15  
 ADO38880  
 ID ADO38880 standard; peptide; 10 AA.  
 XX  
 AC ADO38880;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Human Her-2/neu MHC class II-presented epitope #67.  
 XX  
 KW Antibacterial; Virucide; Fungicide; Antiparasitic; Antiarthritic;  
 KW Antirheumatic; Neuroprotective; Antiinflammatory; Dermatological;  
 KW Immunosuppressive; Antidiabetic; Antithyroid; Antiasthmatic;  
 KW Antiallergic; Cytostatic; Antiproliferative; Gene Therapy; Vaccine;  
 KW MHC Class II; II-key motif; immune response; anthrax; EBOLA; HIV;  
 KW influenza; vaccinia virus; infection; bacterium; virus; parasite; fungus;  
 KW rickettsia; rheumatoid arthritis; multiple sclerosis;  
 KW lupus erythematosus; diabetes mellitus; myasthenia gravis;  
 KW autoimmune thyroiditis; scleroderma; dermatomyositis; pemphigus; asthma;  
 KW allergic rhinitis; topical dermatitis; colitis; cancer; psoriasis;  
 KW adenoma.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2004058881-A1.  
 PN  
 PD 25-MAR-2004.  
 XX  
 PF 24-SEP-2002; 2002US-00253286.  
 XX  
 PR 24-SEP-2002; 2002US-00253286.  
 XX  
 PA (ANTI-) ANTIGEN EXPRESS INC.  
 XX  
 PI Humphreys RE, Xu M;  
 XX  
 XX WPI; 2004-294259/27.  
 DR  
 XX  
 PT New non-naturally occurring protein or polypeptide modified by  
 PT recombinant DNA techniques, useful for treating multiple sclerosis,  
 PT diabetes mellitus, myasthenia gravis, scleroderma, allergic rhinitis,  
 PT colitis, cancer or psoriasis.  
 XX  
 PS Example 16; Page 57; 90pp; English.  
 XX  
 CC The invention relates to a non-naturally occurring protein or polypeptide  
 CC (I) modified by recombinant DNA techniques comprising: a C-terminal  
 CC element comprising an MHC Class II-presented epitope; an N-terminal  
 CC element comprising an II-key motif; and an intervening element comprising  
 CC a sequence of 4-11 amino acid residues where the modification by  
 CC recombinant DNA techniques taking place within elements (b) and (c). Also  
 CC described are methods for: suppressing or enhancing an immune response  
 CC directed toward an MHC (major histocompatibility complex) Class II-  
 CC presented epitope of interest. Suppressing an immune response directed  
 CC toward an MHC Class II-presented epitope of interest comprises: providing  
 CC a nucleic acid sequence encoding the MHC Class II-presented epitope of  
 CC interest, the nucleic acid sequence encoding an II-key motif located 4-11  
 CC amino acids upstream from the N-terminal residue of the MHC Class II-  
 CC presented epitope of interest; and modifying the II-key motif to decrease

CC its conformance to the archetypal II-key regulatory motif. Enhancing an  
 CC immune response directed toward an MHC Class II-presented epitope of  
 CC interest comprises: providing a nucleic acid sequence encoding the MHC  
 CC Class II-presented epitope of interest, the nucleic acid sequence lacking  
 CC an II-key motif located 4-11 amino acids upstream from the N-terminal  
 CC residue of the MHC Class II-presented epitope of interest; and modifying  
 CC the nucleic acid sequence to introduce an II-key motif appropriately  
 CC spaced from the MHC Class II-presented epitope. The protein or  
 CC polypeptide of interest corresponds to a protein or polypeptide encoded  
 CC by an infectious pathogen selected from anthrax, EBOLA, HIV or influenza,  
 CC preferably vaccinia virus. The non-naturally occurring protein or  
 CC polypeptide (I) modified by recombinant DNA techniques is useful for  
 CC treating infectious diseases caused or associated with infection by a  
 CC bacterium, virus, parasite, fungus, rickettsia or other infectious  
 CC agents. It is also useful for treating rheumatoid arthritis, multiple  
 CC sclerosis, lupus erythematosus, diabetes mellitus, myasthenia gravis,  
 CC autoimmune thyroiditis, scleroderma, dermatomyositis, pemphigus, asthma,  
 CC allergic rhinitis, topical dermatitis, colitis, cancer, psoriasis or  
 CC adenomas. The present sequence represents the amino acid sequence of an  
 CC MHC class II-presented epitope used in the invention.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VMAGVGSPYV 10  
 Db 1 VMAGVGSPYV 10  
 |||||

Search completed: April 11, 2006, 19:18:40  
 Job time : 187 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 11, 2006, 19:22:50 ; Search time 46 Seconds  
(without alignments)  
17.973 Million cell updates/sec

Title: US-09-277-064-12

Perfect score: 51

Sequence: 1 VMAGVSPYV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 130918

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5 COMB.pep:\*
- 2: /cgn2\_6/prodata/1/iaa/6 COMB.pep:\*
- 3: /cgn2\_6/prodata/1/iaa/H COMB.pep:\*
- 4: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep:\*
- 5: /cgn2\_6/prodata/1/iaa/RE COMB.pep:\*
- 6: /cgn2\_6/prodata/1/iaa/backfilese1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	1	US-08-467-083-29
2	51	100.0	10	1	US-08-414-417B-29
3	51	100.0	10	1	US-08-486-348A-29
4	51	100.0	10	1	US-08-468-545B-29
5	51	100.0	10	2	US-08-466-680B-29
6	51	100.0	10	2	US-09-341-982-95
7	51	100.0	10	2	US-09-543-608A-16
8	51	100.0	10	2	US-09-354-533-29
9	51	100.0	10	4	PCT-US95-16415-12
10	47	92.2	9	2	US-09-527-487-9
11	47	92.2	10	2	US-08-159-339A-263
12	29	56.9	9	1	US-08-725-736D-10
13	29	56.9	9	2	US-09-162-368B-10
14	29	56.9	9	2	US-09-161-877B-10
15	27	52.9	10	1	US-08-172-707-5
16	27	52.9	10	1	US-08-412-865-5
17	27	52.9	10	1	US-08-476-505-5
18	27	52.9	10	1	US-08-487-396-5
19	27	52.9	10	1	US-08-941-553-5
20	27	52.9	10	2	US-08-769-143-5
21	26	51.0	9	1	US-08-725-736D-9
22	26	51.0	9	2	US-09-162-368B-9
23	26	51.0	9	2	US-09-162-368B-28
24	26	51.0	9	2	US-09-161-877B-9
25	26	51.0	9	2	US-09-161-877B-28
26	25	49.0	8	2	US-09-082-737-12
27	25	49.0	8	2	US-09-718-032-12

28 25 49.0 9 1 US-08-725-736D-8 Sequence 8, Appli  
29 25 49.0 9 1 US-08-725-736D-14 Sequence 14, Appli  
30 25 49.0 9 1 US-08-318-856A-36 Sequence 36, Appli  
31 25 49.0 9 2 US-09-162-368B-8 Sequence 8, Appli  
32 25 49.0 9 2 US-09-162-368B-14 Sequence 14, Appli  
33 25 49.0 9 2 US-09-162-368B-31 Sequence 31, Appli  
34 25 49.0 9 2 US-09-161-877B-8 Sequence 8, Appli  
35 25 49.0 9 2 US-09-161-877B-14 Sequence 14, Appli  
36 25 49.0 9 2 US-09-161-877B-31 Sequence 31, Appli  
37 25 49.0 10 2 US-09-100-930A-14 Sequence 14, Appli  
38 24 47.1 7 2 US-08-861-153A-28 Sequence 28, Appli  
39 24 47.1 8 2 US-09-239-043D-4 Sequence 4, Appli  
40 24 47.1 8 2 US-09-239-043D-1321 Sequence 1321, Ap  
41 24 47.1 9 1 US-08-725-736D-4 Sequence 4, Appli  
42 24 47.1 9 1 US-08-725-736D-7 Sequence 7, Appli  
43 24 47.1 9 1 US-08-725-736D-11 Sequence 11, Appli  
44 24 47.1 9 2 US-08-880-963-8 Sequence 8, Appli  
45 24 47.1 9 2 US-09-162-368B-4 Sequence 4, Appli

## ALIGNMENTS

## RESULT 1

US-08-467-083-29  
; Sequence 29, Application US/08467083  
; Patent No. 5726023  
; GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.

APPLICANT: Disis, Mary L.

TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN

TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSER: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,083

FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/414,417.

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 920010.448C2

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

TELEX: 3723836 SEEDANBERRY

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-467-083-29

Query Match

Best Local Similarity 100.0%; Score 51; DB 1; Length 10;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VMAGVGSPPV 10.
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Db 1 VMAGVGSPPV 10

RESULT 2
US-08-414-417B-29
; Sequence 29, Application US/08414417B
; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-414-417B-29

Query Match 100.0%; Score 51; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10
    |||||
Db 1 VMAGVGSPPV 10

RESULT 3
US-08-486-348A-29
; Sequence 29, Application US/08486348A
; Patent No. 584538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
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QY 1 VMAGVGSPPV 10
    |||||
Db 1 VMAGVGSPPV 10

RESULT 4
US-08-468-545B-29
; Sequence 29, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,545B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-486-348A-29

Query Match 100.0%; Score 51; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10
    |||||
Db 1 VMAGVGSPPV 10

RESULT 4
US-08-468-545B-29
; Sequence 29, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,545B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
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; TOPOLOGY: linear
US-08-468-545B-29
Query Match      100.0%; Score 51; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VMAGVGSPPV 10
DB      1 VMAGVGSPPV 10

RESULT 5
US-08-466-680B-29
; Sequence 29, Application US/08466680B
; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,680B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-466-680B-29

Query Match      100.0%; Score 51; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VMAGVGSPPV 10
DB      1 VMAGVGSPPV 10

RESULT 6
US-09-341-982-95
; Sequence 95, Application US/09341982
; Patent No. 6558671
; GENERAL INFORMATION:
; APPLICANT: SLINGLUFF, Craig L.
; APPLICANT: HUNT, Donald F.
; APPLICANT: ENGELHARD, Victor H.
; APPLICANT: KITTLESEN, David
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
```

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; TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR
; FILE REFERENCE: SLINGLUFF-3B
; CURRENT APPLICATION NUMBER: US/09/341,982
; CURRENT FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: PCT/US98/01592
; EARLIER FILING DATE: 1998-01-29
; EARLIER APPLICATION NUMBER: 60/037,781
; EARLIER FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 95
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
; OTHER INFORMATION: human protein
US-09-341-982-95
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Query Match      100.0%; Score 51; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 VMAGVGSPPV 10
DB      1 VMAGVGSPPV 10
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RESULT 7
US-09-543-608A-16,
; Sequence 16, Application US/09543608A
; Patent No. 6602510
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa A.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen
; TITLE OF INVENTION: Peptides and Vaccine Compositions
; FILE REFERENCE: 018623-015710US
; CURRENT APPLICATION NUMBER: US/09/543,608A
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Her2/neu.773
US-09-543-608A-16
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Query Match      100.0%; Score 51; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 VMAGVGSPPV 10
DB      1 VMAGVGSPPV 10
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RESULT 8
US-09-354-533-29
; Sequence 29, Application US/09354533
; Patent No. 6664370
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
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```

; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; HER-2/neu ONCOGENE IS ASSOCIATED
;
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 15-Jul-1999
; APPLICATION NUMBER: US/09/354,533
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
;
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-354-533-29

Query Match 100.0%; Score 51; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVSPYV 10
DB 1 VMAGVSPYV 10

RESULT 9
PCT-US95-16415-12
; Sequence 12, Application PC/TUS9516415
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10666 North Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/16415
; FILING DATE: 13-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/355,558
; FILING DATE: 14-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Logan, April C.

;
; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; HER-2/neu ONCOGENE IS ASSOCIATED
;
; NUMBER OF SEQUENCES: 33,950
; REFERENCE/DOCKET NUMBER: 433.1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-16415-12

Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVSPYV 10
DB 1 VMAGVSPYV 10

RESULT 10
US-09-527-487-9
; Sequence 9, Application US/09527487
; Patent No. 6528060
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
; FILE REFERENCE: 126881309200
; CURRENT APPLICATION NUMBER: US/09/527,487
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-527-487-9

Query Match 92.2%; Score 47; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VMAGVSPYV 10
DB 1 VMAGVSPYV 9

RESULT 11
US-08-159-339A-263
; Sequence 263, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
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;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/159,339A  
;; FILING DATE: 29-NOV-1993  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/926,666  
;; FILING DATE: 07-AUG-1992  
;; APPLICATION NUMBER: US 08/027,746  
;; FILING DATE: 05-MAR-1993  
;; APPLICATION NUMBER: US 08/103,396  
;; FILING DATE: 06-AUG-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Weber, Ellen Lauver  
;; REGISTRATION NUMBER: 32,762  
;; REFERENCE/DOCKET NUMBER: 018623-005030US  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 263:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-159-339A-263

Query Match 92.2%; Score 47; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.048; 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0

QY 1 VNAGVGSPPY 9  
Db 2 VNAGVGSPPY 10

RESULT 12  
US-08-725-736D-10  
; Sequence 10, Application US/08725736D  
; Patent No. 5831016  
; GENERAL INFORMATION:  
; APPLICANT: WANG, R.F.; ROSENBERG, S. A.  
; TITLE OF INVENTION: IDENTIFICATION OF TRP-2 AS  
; TITLE OF INVENTION: A HUMAN TUMOR ANTIGEN RECOGNIZED BY CYTOTOXIC T  
; TITLE OF INVENTION: LYMPHOCYTES  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/725,736D  
; FILING DATE: 04-OCT-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/599,602  
; FILING DATE: 09-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DOROTHY R. AUTH  
; REGISTRATION NUMBER: 36,434  
; REFERENCE/DOCKET NUMBER: 2076-4243  
; TELEPHONE: (212) 751-6800  
; TELEFAX: (212) 751-6849

;; TELEX: 421792  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9  
;; TYPE: AMINO ACID  
;; STRANDEDNESS: SINGLE  
;; TOPOLOGY: UNKNOWN  
;; MOLECULE TYPE: PEPTIDE  
;; DESCRIPTION: PEPTIDE  
;; FEATURE:  
;; NAME/KEY: TRP-2 PEPTIDE VARIANT  
;; LOCATION:  
;; IDENTIFICATION METHOD:  
;; OTHER INFORMATION:  
;; US-08-725-736D-10

Query Match 56.9%; Score 29; DB 1; Length 9;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 MAGVGSPPY 9  
Db 1 LAGPGRPY 8

RESULT 13  
US-09-162-368B-10  
; Sequence 10, Application US/09162368B  
; Patent No. 6083703  
; GENERAL INFORMATION:  
; APPLICANT: WANG, R.F.; ROSENBERG, S. A.  
; TITLE OF INVENTION: IDENTIFICATION OF TRP-2 AS  
; TITLE OF INVENTION: A HUMAN TUMOR ANTIGEN RECOGNIZED BY CYTOTOXIC T  
; TITLE OF INVENTION: LYMPHOCYTES  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MICROSOFT WORD 97  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/162,368B  
; FILING DATE: 28-SEPT-1998  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/725,736  
; FILING DATE: 04-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/599,602  
; FILING DATE: 09-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KATHRYN M. BROWN  
; REGISTRATION NUMBER: 34,556  
; REFERENCE/DOCKET NUMBER: 2026-4243US1  
; TELEPHONE: (212) 751-6849  
; TELEFAX: (212) 751-6849  
; TELEX: 421792  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9  
; TYPE: AMINO ACID  
; STRANDEDNESS: SINGLE  
; TOPOLOGY: UNKNOWN  
; MOLECULE TYPE: PEPTIDE  
; DESCRIPTION: PEPTIDE

;; FEATURE:  
;; NAME/KEY: TRP-2 PEPTIDE VARIANT  
;; LOCATION:  
;; IDENTIFICATION METHOD:  
;; OTHER INFORMATION:  
US-09-162-3688-10

Query Match 56.9%; Score 29; DB 2; Length 9;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 MAGVGSPPY 9  
DB 1 LAGPGRPY 8

RESULT 14  
US-09-161-8778-10  
; Sequence 10, Application US/09161877B  
; Patent No. 6132980  
; GENERAL INFORMATION:  
; APPLICANT: WANG, R.F.; ROSENBERG, S. A.  
; TITLE OF INVENTION: IDENTIFICATION OF TRP-2  
; TITLE OF INVENTION: AS A HUMAN TUMOR ANTIGEN RECOGNIZED BY  
; TITLE OF INVENTION: CYTOTOXIC T LYMPHOCYTES  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MICROSOFT WORD 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/161,877B  
FILING DATE: 28-SEPT-1998  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/725,736  
FILING DATE: 04-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/599,602  
FILING DATE: 09-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: KATHRYN M. BROWN  
REGISTRATION NUMBER: 34,556  
REFERENCE/DOCKET NUMBER: 2026-4243US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9  
TYPE: AMINO ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: UNKNOWN  
MOLECULE TYPE:  
DESCRIPTION: PEPTIDE  
FEATURE:  
NAME/KEY: TRP-2 PEPTIDE VARIANT  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
US-09-161-8778-10

Query Match 56.9%; Score 29; DB 2; Length 9;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 MAGVGSPPY 9  
DB 1 LAGPGRPY 8

RESULT 15  
US-08-172-707-5  
; Sequence 5, Application US/08172707  
; Patent No. 5455168  
; GENERAL INFORMATION:  
; APPLICANT: MARUTA, Kazuhiko  
; APPLICANT: KUBOTA, Michio  
; APPLICANT: SUGIMOTO, Toshiyuki  
; TITLE OF INVENTION: NON-REDUCING SACCHARIDE-FORMING ENZYME,  
; TITLE OF INVENTION: AND ITS PREPARATION AND USES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/172,707  
FILING DATE: 12-DEC-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 362131/1992  
FILING DATE: 28-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 265416/1993  
FILING DATE: 30-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: TOWNSEND, G. Kevin  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MARUTA-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-172-707-5

Query Match 52.9%; Score 27; DB 1; Length 10;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GVGSPY 9  
DB 2 GRGSPY 7

Search completed: April 11, 2006, 19:24:09  
JOB time : 46 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 11, 2006, 19:23:29 ; Search time 163 Seconds  
(without alignments)  
25.634 Million cell updates/sec

Title: US-09-277-064-12

Perfect score: 51

Sequence: 1 VMAGVGSPPV 10

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 232507

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgm2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgm2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgm2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgm2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgm2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgm2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	2	US-08-812-393A-49
2	51	100.0	10	3	US-09-354-533-29
3	51	100.0	10	3	US-09-277-074-12
4	51	100.0	10	3	US-09-277-064-12
5	51	100.0	10	3	US-09-774-681-49
6	51	100.0	10	4	US-10-080-013-16
7	51	100.0	10	4	US-10-245-871-620
8	51	100.0	10	4	US-10-149-138-786
9	51	100.0	10	4	US-10-149-138-2352
10	51	100.0	10	4	US-10-149-138-4335
11	51	100.0	10	4	US-10-149-138-4422
12	51	100.0	10	4	US-10-149-138-4435
13	51	100.0	10	4	US-10-253-286-620
14	51	100.0	10	4	US-10-289-566-16
15	51	100.0	10	4	US-10-333-430-31
16	51	100.0	10	4	US-10-647-005-29
17	51	100.0	10	4	US-10-149-138-786
18	51	100.0	10	4	US-10-149-138-2352
19	51	100.0	10	4	US-10-149-138-4335
20	51	100.0	10	4	US-10-149-138-4422
21	51	100.0	10	4	US-10-149-138-4435
22	51	100.0	10	6	US-11-121-347-29
23	47	92.2	9	4	US-10-338-730-9
24	47	92.2	9	4	US-10-149-138-60
25	47	92.2	9	4	US-10-149-138-520
26	47	92.2	9	4	US-10-149-138-1413
27	47	92.2	9	4	US-10-149-138-1891

28	47	92.2	9	4	US-10-149-138-2351	Sequence 2351, Ap
29	47	92.2	9	4	US-10-149-138-2441	Sequence 2441, Ap
30	47	92.2	9	4	US-10-149-138-3129	Sequence 3129, Ap
31	47	92.2	9	4	US-10-149-138-3616	Sequence 3616, Ap
32	47	92.2	9	4	US-10-149-138-3962	Sequence 3962, Ap
33	47	92.2	9	4	US-10-149-138-60	Sequence 60, Appl
34	47	92.2	9	4	US-10-149-138-520	Sequence 520, Appl
35	47	92.2	9	4	US-10-149-138-1413	Sequence 1413, Ap
36	47	92.2	9	4	US-10-149-138-1891	Sequence 1891, Ap
37	47	92.2	9	4	US-10-149-138-2351	Sequence 2351, Ap
38	47	92.2	9	4	US-10-149-138-2441	Sequence 2441, Ap
39	47	92.2	9	4	US-10-149-138-3129	Sequence 3129, Ap
40	47	92.2	9	4	US-10-149-138-3616	Sequence 3616, Ap
41	47	92.2	9	4	US-10-149-138-3962	Sequence 3962, Ap
42	47	92.2	10	4	US-10-149-138-97	Sequence 97, Appl
43	47	92.2	10	4	US-10-149-138-1455	Sequence 1455, Ap
44	47	92.2	10	4	US-10-149-138-2385	Sequence 2385, Ap
45	47	92.2	10	4	US-10-149-138-3174	Sequence 3174, Ap

#### ALIGNMENTS

#### RESULT 1

US-08-812-393A-49

; Sequence 49, Application US/0812393A

; Publication No. US20010007152A1

; GENERAL INFORMATION:

; APPLICANT: SHERMAN, Linda A.

; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING

; TITLE OF INVENTION: T CELL RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR

; TITLE OF INVENTION: ANTIGENS

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESS: MORRISON & FOERSTER

; STREET: 2000 Pennsylvania Avenue, NW, suite 5500

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20006-1888

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/812.393A

; FILING DATE: 05-MAR-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Murashige, Kate H

; REGISTRATION NUMBER: 29, 959

; REFERENCE/DOCKET NUMBER: 31333-20001.00

; TELEPHONE: 202-887-1500

; TELEFAX: 202-822-0168

; TELEX:

; INFORMATION FOR SEQ ID NO: 49:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-812-393A-49

Query Match

Best Local Similarity 100.0%; Score 51; DB 2; Length 10;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
Db 1 VMAGVGSPPV 10

## RESULT 2

US-09-354-533-29

; Sequence 29, Application US/09354533

; Publication No. US20020055614A1

; GENERAL INFORMATION:

; APPLICANT: Cheever, Martin A.

; Disis, Mary L.

; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN

; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE

; HER-2/neu ONCOGENE IS ASSOCIATED

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; City: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/354,533

; FILING DATE: 15-Jul-1999

; CLASSIFICATION: &lt;Unknown&gt;

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharkey, Richard G.

; REGISTRATION NUMBER: 32,629

; REFERENCE/DOCKET NUMBER: 920010.448C9

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 29:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; STRANDEDNESS: &lt;Unknown&gt;

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 29:

US-09-354-533-29

Query Match 100.0%; Score 51; DB 3; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10

Db 1 VMAGVGSPPV 10

## RESULT 3

US-09-277-074-12

; Sequence 12, Application US/09277074

; Publication No. US2003022820A1

; GENERAL INFORMATION:

; APPLICANT: Sherman, Linda A.

; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS

; FILE REFERENCE: SCR2155S

; CURRENT APPLICATION NUMBER: US/09/277,074

; CURRENT FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 08/355,558

; PRIOR FILING DATE: 1994-12-14

; PRIOR APPLICATION NUMBER: PCT/US95/16415

; PRIOR FILING DATE: 1995-12-14

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 12  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-277-074-12

Query Match 100.0%; Score 51; DB 3; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10

Db 1 VMAGVGSPPV 10

## RESULT 4

US-09-277-064-12

; Sequence 12, Application US/09277064

; Publication No. US20030064916A1

; GENERAL INFORMATION:

; APPLICANT: Sherman, Linda A.

; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS

; FILE REFERENCE: SCR2152S

; CURRENT APPLICATION NUMBER: US/09/277,064

; CURRENT FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 08/355,558

; PRIOR FILING DATE: 1994-12-14

; PRIOR APPLICATION NUMBER: PCT/US95/16415

; PRIOR FILING DATE: 1995-12-14

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 12

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-277-064-12

Query Match 100.0%; Score 51; DB 3; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10

Db 1 VMAGVGSPPV 10

## RESULT 5

US-09-774-681-49

; Sequence 49, Application US/09774681

; Publication No. US20030208780A1

; GENERAL INFORMATION:

; APPLICANT: Sunol Molecular Corporatiopn

; APPLICANT: Lustgarten, Joseph

; APPLICANT: Sherman, Linda

; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING T CELL

; RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS

; FILE REFERENCE: 31333-20001.01

; CURRENT APPLICATION NUMBER: US/09/774,681

; CURRENT FILING DATE: 2001-02-01

; PRIOR APPLICATION NUMBER: US 08/812,393

; PRIOR FILING DATE: 1997-03-05

; PRIOR APPLICATION NUMBER: US 60/012,845

; PRIOR FILING DATE: 1996-03-05

; NUMBER OF SEQ ID NOS: 65

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 49

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthesized peptide

US-09-774-681-49

Query Match 100.0%; Score 51; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.016; 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
DB 1 VMAGVGSPPV 10

## RESULT 6

US-10-080-013-16  
; Sequence 16, Application US/10080013  
; Publication No. US2003007248A1

; GENERAL INFORMATION:

; APPLICANT: Moriarty, Ann

; APPLICANT: Leturcq, Didier

; APPLICANT: Degraw, Juli

; APPLICANT: Heiskala, Marja

; APPLICANT: Peterson, Per

; APPLICANT: Jackson, Michael

; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS

; FILE REFERENCE: ORT-1557

; CURRENT APPLICATION NUMBER: US/10/080,013

; CURRENT FILING DATE: 2002-02-19

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 16

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-080-013-16

Query Match 100.0%; Score 51; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.016; 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
DB 1 VMAGVGSPPV 10

## RESULT 7

US-10-245-871-620

; Sequence 620, Application US/10245871

; Publication No. US20030235594A1

; GENERAL INFORMATION:

; APPLICANT: HUMPHREYS, ROBERT

; APPLICANT: XU, MINZHEN

; TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

; FILE REFERENCE: REH-2013

; CURRENT APPLICATION NUMBER: US/10/245,871

; CURRENT FILING DATE: 2003-01-09

; PRIOR APPLICATION NUMBER: 10/197,000

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: 09/396,813

; PRIOR FILING DATE: 1999-09-14

; NUMBER OF SEQ ID NOS: 905

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 620

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-245-871-620

Query Match 100.0%; Score 51; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.016; 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
DB 1 VMAGVGSPPV 10

## RESULT 8

US-10-149-138-786

; Sequence 786, Application US/10149138

; Publication No. US20040018971A1

; GENERAL INFORMATION:

; APPLICANT: Fikes, John

; APPLICANT: Sette, Alessandro

; APPLICANT: Sidney, John

; APPLICANT: Southwood, Scott

; APPLICANT: Chesnut, Robert

; APPLICANT: Celis, Esteban

; APPLICANT: Keogh, Elissa

; TITLE OF INVENTION: Inducing Cellular Immune Responses to

; FILE REFERENCE: 2060.0140001

; CURRENT APPLICATION NUMBER: US/10/149,138

; CURRENT FILING DATE: 2002-06-10

; PRIOR APPLICATION NUMBER: PCT/US00/33591

; PRIOR FILING DATE: 2000-12-11

; PRIOR APPLICATION NUMBER: US 09/458,299

; PRIOR FILING DATE: 1999-12-11

; NUMBER OF SEQ ID NOS: 4641

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 786

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Artificially Synthesized Peptide

US-10-149-138-786

Query Match 100.0%; Score 51; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.016; 0; Indels 0; Gaps 0;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10  
DB 1 VMAGVGSPPV 10

## RESULT 9

US-10-149-138-2352

; Sequence 2352, Application US/10149138

; Publication No. US20040018971A1

; GENERAL INFORMATION:

; APPLICANT: Fikes, John

; APPLICANT: Sette, Alessandro

; APPLICANT: Sidney, John

; APPLICANT: Southwood, Scott

; APPLICANT: Chesnut, Robert

; APPLICANT: Celis, Esteban

; APPLICANT: Keogh, Elissa

; TITLE OF INVENTION: Inducing Cellular Immune Responses to

; FILE REFERENCE: 2060.0140001

; CURRENT APPLICATION NUMBER: US/10/149,138

; CURRENT FILING DATE: 2002-06-10

; PRIOR APPLICATION NUMBER: PCT/US00/33591

; PRIOR FILING DATE: 2000-12-11

; PRIOR APPLICATION NUMBER: US 09/458,299

; PRIOR FILING DATE: 1999-12-11

; NUMBER OF SEQ ID NOS: 4641

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 2352

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Artificially Synthesized Peptide

US-10-149-138-2352

Query Match 100.0%; Score 51; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.016; 0; Indels 0; Gaps 0;

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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10
   |||||
Db 1 VMAGVGSPPV 10

RESULT 10
US-10-149-138-4335
; Sequence 4335, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4335
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4335

Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10
   |||||
Db 1 VMAGVGSPPV 10

RESULT 11
US-10-149-138-4422
; Sequence 4422, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4422
; LENGTH: 10
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4422

Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10
   |||||
Db 1 VMAGVGSPPV 10

RESULT 12
US-10-149-138-4435
; Sequence 4435, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4435
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4435

Query Match 100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMAGVGSPPV 10
   |||||
Db 1 VMAGVGSPPV 10

RESULT 13
US-10-253-286-620
; Sequence 620, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: 11-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 620
; LENGTH: 10
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-286-620

Query Match      100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VMAGVGSPYV 10
Db      1 VMAGVGSPYV 10
|||||

RESULT 14
US-10-289-566-16
; Sequence 16, Application US/10289566
; Publication No. US20040071671A1
; GENERAL INFORMATION:
; APPLICANT: Leturcq, Didier J.
; APPLICANT: Moriarty, Ann M.
; APPLICANT: Jackson, Michael R.
; APPLICANT: Peterson, Per A.
; APPLICANT: Richards, Jon M.
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT 1342CIP
; CURRENT APPLICATION NUMBER: US/10/289,566
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/270,252
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: US 10/080,013
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-289-566-16

Query Match      100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VMAGVGSPYV 10
Db      1 VMAGVGSPYV 10
|||||

; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-333-430-31

Query Match      100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VMAGVGSPYV 10
Db      1 VMAGVGSPYV 10
|||||

Search completed: April 11, 2006, 19:26:58
Job time : 164 secs

RESULT 15
US-10-333-430-31
; Sequence 31, Application US/10333430
; Publication No. US20040072240A1
; GENERAL INFORMATION:
; APPLICANT: INSERM
; APPLICANT: INSTITUT GUSTAVE ROUSSY
; APPLICANT: KOSMATOPOULOS, Kostas
; APPLICANT: TOURDOT, Sophie
; APPLICANT: SCARDINO, Antonio
; APPLICANT: GROSS, David, Alexandre
; TITLE OF INVENTION: METHOD FOR SCREENING PEPTIDES FOR USE IN
; TITLE OF INVENTION: IMMUNOTHERAPY
; FILE REFERENCE: 33339/259034
; CURRENT APPLICATION NUMBER: US/10/333,430
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: FR 0009591
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
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